

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:40:49 ; Search time 84 Seconds
(without alignments)
225.559 Million cell updates/sec

Title: US-09-674-496D-6

Perfect score: 217

Sequence: 1 ASNGVCSPEMPGCTGACRCIPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	130	1	AL1F_PEA
2	216	99.5	130	1	AL1A_PEA
3	212	97.7	130	1	AL1D_PEA
4	210	96.8	130	1	AL1E_PEA
5	207	95.4	130	1	AL1B_PEA
6	194	89.4	96	2	Q6A1C7
7	173	79.7	130	1	AL1C_PEA
8	159	73.3	98	2	Q6A1B4
9	159	73.3	100	2	Q7XZC3
10	156	71.9	119	1	ALB1_GLYSO
11	156	71.9	140	2	Q7XZC5
12	155	71.4	100	2	Q6A1D7
13	154	71.0	119	1	ALB1_SOYBN
14	153.5	70.7	90	1	ALB1_PHAAN
15	153	70.5	89	1	ALB1_PHAU
16	153	70.5	98	2	Q6A1C9
17	149	68.7	99	2	Q6A1C8
18	148.5	68.4	101	2	Q6A1D1
19	146.5	67.5	101	2	Q6A1D3
20	143.5	66.1	109	2	Q7XZC2
21	138	63.6	99	2	Q6A1D5
22	134	61.8	91	2	Q6A1D6
23	132	60.8	98	2	Q6A1D2
24	130	59.9	142	2	Q7XZC4
25	104.5	48.2	101	2	Q6A1D0
26	100	46.1	59	2	Q6A1C3
27	89	41.0	81	1	ALB1_LUPAN
28	87	40.1	58	2	Q6A1C4
29	86	39.6	58	2	Q6A1B9
30	82	39.2	60	2	Q6A1C1
31	82	37.8	58	2	Q6A1C5

ALIGNMENTS

32	73.5	33.9	1642	2	O62055	O62055 caenorhabdi
33	72	33.2	58	2	O6A1C0	O6A1C0 vigna subte
34	69	31.8	536	2	O8I1D9	O8I1D9 drosophila
35	69	31.8	539	2	O8M1S4	O8M1S4 drosophila
36	67	30.9	59	2	O6A1C6	O6A1C6 bituminaria
37	65	30.0	1024	2	O9BX11	O9BX11 homo sapien
38	65	30.0	1104	1	NFX1_HUMAN	NFX1_HUMAN homo sapien
39	65	30.0	1120	1	O96EL5	O96EL5 homo sapien
40	64	29.5	215	2	O9D7N2	O9D7N2 mus musculus
41	62.5	28.8	257	2	O6PQG7	O6PQG7 phytophthor
42	62.5	28.8	583	1	AXU1_MOUSE	AXU1_MOUSE mus musculus
43	61	28.1	96	2	O9LJQ3	O9LJQ3 arabidopsis
44	60	27.6	61	1	MT1A_BOVIN	MT1A_BOVIN bos taurus
45	60	27.6	61	1	MT1B_SHEEP	MT1B_SHEEP ovis aries
46	60	27.6	61	1	MT1C_SHEEP	MT1C_SHEEP ovis aries
47	60	27.6	61	1	MT1C_SHEEP	MT1C_SHEEP ovis aries
48	60	27.6	61	2	O8M1I4	O8M1I4 bos taurus
49	60	27.6	61	2	O6R522	O6R522 bos mutus g
50	60	27.6	249	2	O917N9	O917N9 la piedada-m
51	60	27.6	1785	2	O8JHV7	O8JHV7 brachydanio
52	59.5	27.4	79	1	LC81_ARATH	LC81_ARATH arabidopsis
53	59.5	27.4	675	2	O7QS27	O7QS27 giardia lam
54	59.5	27.4	685	2	O7QWD9	O7QWD9 giardia lam
55	59	27.2	297	2	O6DH56	O6DH56 brachydanio
56	59	27.2	420	2	O6NM65	O6NM65 brachydanio
57	59	27.2	1799	1	LMB2_MOUSE	LMB2_MOUSE mus musculus
58	59	27.2	1799	2	O8R0Y0	O8R0Y0 mus musculus
59	59	27.2	3775	2	O7PMF9	O7PMF9 anopheles g
60	58.5	27.0	149	2	O6PQH2	O6PQH2 phytophthor
61	58.5	27.0	749	2	O86TP7	O86TP7 homo sapien
62	58.5	27.0	804	2	O7TFT4	O7TFT4 mus musculus
63	58.5	27.0	818	2	O8CC59	O8CC59 mus musculus
64	58.5	27.0	818	2	O9DBC8	O9DBC8 mus musculus
65	58.5	27.0	1035	2	O7QR01	O7QR01 giardia lam
66	58.5	27.0	1114	2	O9JKW7	O9JKW7 mus musculus
67	58.5	27.0	1761	2	O86XN2	O86XN2 homo sapien
68	58	26.7	60	2	O6A1C2	O6A1C2 mundulea se
69	58	26.7	285	2	O7VBZ4	O7VBZ4 prochloroco
70	58	26.7	418	2	O8LNM4	O8LNM4 oryza sativ
71	58	26.7	1801	1	LMB2_RAT	LMB2_RAT rattus norv
72	58	26.7	23015	2	O8I0I8	O8I0I8 drosophila
73	57	26.3	174	1	CYS3_OSTOS	CYS3_OSTOS ostertagia
74	57	26.3	194	2	O9N9C6	O9N9C6 ostertagia
75	57	26.3	291	2	O8MKQ8	O8MKQ8 drosophila
76	56.5	26.0	271	1	K105_HUMAN	K105_HUMAN homo sapien
77	56.5	26.0	277	2	O6V4H5	O6V4H5 procambatus
78	56.5	26.0	1156	2	O963T3	O963T3 aedes aegyp
79	56	25.8	56	1	M87F_DROME	M87F_DROME drosophila
80	56	25.8	61	1	MT1_BOVIN	MT1_BOVIN bos taurus
81	56	25.8	194	2	O7PI78	O7PI78 anopheles g
82	56	25.8	264	2	O66T09	O66T09 brachydanio
83	56	25.8	270	1	DAPF_RICPR	DAPF_RICPR rickettsia
84	56	25.8	274	2	O6W4T8	O6W4T8 brachydanio
85	56	25.8	302	2	O96H92	O96H92 homo sapien
86	56	25.8	358	2	O8K2C1	O8K2C1 mus musculus
87	56	25.8	375	2	O20002	O20002 caenorhabdi
88	56	25.8	388	2	O6PJL7	O6PJL7 homo sapien
89	56	25.8	405	2	O8S260	O8S260 drosophila
90	56	25.8	426	2	O67U09	O67U09 oryza sativ
91	56	25.8	429	2	O8MUJ9	O8MUJ9 homo sapien
92	56	25.8	435	2	O7YR70	O7YR70 canis famli
93	56	25.8	452	1	AAMP_HUMAN	AAMP_HUMAN homo sapien
94	56	25.8	525	2	O6X1X4	O6X1X4 feldmannia
95	56	25.8	609	2	O7QNX8	O7QNX8 giardia lam
96	56	25.8	813	1	YTOJ_CAEEL	YTOJ_CAEEL caenorhabdi
97	55.5	25.6	131	2	O86K22	O86K22 dictyosteli
98	55.5	25.6	747	2	O8VHF4	O8VHF4 mus musculus
99	55.5	25.6	1004	2	O8CGA7	O8CGA7 mus musculus
100	55.5	25.6	1034	2	O8VHL7	O8VHL7 mus musculus

```

RESULT 1
AL1F_PEA
ID AL1F_PEA STANDARD; PRT; 130 AA.
AC P62931; P08687; Q40999; Q7X9N3; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 F precursor (PAL F) (PaaAlb005/PaaAlb011) [Contains: Albumin
1 F chain b (PALb F) (Leginsulin F); Albumin 1 F chain a (PALa F)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Frisson; TISSUE=Seed;
RA Louis S., Delobel B., Gressent F., Rahloui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
from four legume species.";
RL plant Sci. 167:705-714(2004).
RN [2]
RP SEQUENCE OF 27-63, AND FUNCTION.
RA Delobel B., Grenier A., Gueguen J., Ferrasson E., Mbailao M.;
RT "Use of a polypeptide derived from a PALb legume albumen as
insecticide.";
RL Patent number WO9958695, 07-MAY-1999.
RN [3]
RP STRUCTURE BY NMR OF 27-63, AND DISULFIDE BONDS.
RX PubMed=14556622; DOI=10.1021/bi0348031;
RA Jouvencal L., Quillien L., Ferrasson E., Rahbe Y., Gueguen J.,
RA Jovelle F.;
RT "PALb, an insecticidal protein extracted from pea seeds (Pisum
sativum): 1H-2-D NMR study and molecular modeling.";
RL Biochemistry 42:11915-11923(2003).
RN [4]
RP FUNCTION.
RX PubMed=12755698;
RA Gressent F., Rahloui I., Rahbe Y.;
RT "Characterization of a high-affinity binding site for the pea albumin
1b endomotoxin in the weevil Sitophilus.";
RL Eur. J. Biochem. 270:2429-2435(2003).
CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
phosphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
peptide (By similarity). Toxic to various insects through binding
to a high affinity binding site in the insect gut.
CC -1- PTM: The C-terminal glycine may be removed from PALb.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sb-sib.ch).
CC -----
DR EMBL; AJ574793; CAS00465.1; -
DR FDB; IP85; NMR; A=27-63.
DR InterPro; IPR011036; PH related.
KW 3D-structure; Direct protein sequencing; Plant toxin;
KW Seed storage protein; Signal.
FT SIGNAL 1 26 Albumin 1 F chain b.
FT CHAIN 27 63 Potential.
FT PROPEP 64 69 Potential.
FT CHAIN 70 122 Albumin 1 F chain a.
FT PROPEP 123 130 Potential.
FT DISULFID 29 46 By similarity.
FT DISULFID 33 48 By similarity.
FT DISULFID 41 58 By similarity.
SQ SEQUENCE 130 AA; 13912 MW; 1371D80F333E0EFF CRC64;
Query Match 99.5%; Score 216; DB 1; Length 130;
Best Local Similarity 97.3%; Pred. No. 2e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 ASCNGVCSPPFEMPCCGTSACRCIPVGLVIGYCRNPSG 37
QY
27 ASCNGVCSPPFEMPCCGTSACRCIPVGLVIGYCRNPSG 63
DB

RESULT 2
AL1A_PEA
ID AL1A_PEA STANDARD; PRT; 130 AA.
AC P62926; P08687; Q40999; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 A precursor (PAL A) [Contains: Albumin 1 A chain b (PALb A)
(Leginsulin A); Albumin 1 A chain a (PALa A)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Greenfeast; TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kott A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
phosphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
peptide. Toxic to various insects through binding to a high
affinity binding site in the insect gut (By similarity).
CC -1- TISSUE SPECIFICITY: Major component of both the cotyledons and
embryonic axes of mature seeds.
CC -1- DEVELOPMENTAL STAGE: Increasing expression during seed development
followed by a rapid degradation during the first days of seed
germination.
CC -1- PTM: The C-terminal glycine may be removed from PALb.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sb-sib.ch).
CC -----
DR EMBL; M13709; AAA33638.1; -
DR FIR; A25014; A25014.
DR InterPro; IPR011036; PH related.
KW Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 63 Albumin 1 A chain b.
FT PROPEP 64 69 Potential.
FT CHAIN 70 122 Albumin 1 A chain a.
FT PROPEP 123 130 Potential.
FT DISULFID 29 46 By similarity.
FT DISULFID 33 48 By similarity.
FT DISULFID 41 58 By similarity.
SQ SEQUENCE 130 AA; 13912 MW; 1371D80F333E0EFF CRC64;
Query Match 99.5%; Score 216; DB 1; Length 130;
Best Local Similarity 97.3%; Pred. No. 2e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 ASCNGVCSPPFEMPCCGTSACRCIPVGLVIGYCRNPSG 37
QY
```

[illegible]

27 ASCNGVCSPPFMPGCGSSACRCIPVGLVGYCRHPSG 63

```

RESULT 5
AL1B_PEA
ID AL1B_PEA STANDARD; Q04999; Q9M3X4; PRT; 130 AA.
AC P62927; P08687; Q04999; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 B precursor (PA1 B) [Contains: Albumin 1 B chain b (PA1B B)
DE (Leghemin B); Albumin 1 B chain a (PA1A B)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Greenfeast; TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Birte; TISSUE=Cotyledon;
RA Domoney C., Ellis N., Wellham T.;
RT "Genetic loci controlling albumin synthesis in Pisum.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PA1B binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide. Toxic to various insects through binding to a high
CC affinity binding site in the insect gut (by similarity).
CC -!- TISSUE SPECIFICITY: Major component of both the cotyledons and
CC embryonic axes of mature seeds.
CC -!- DEVELOPMENTAL STAGE: Increasing expression during seed development
CC followed by a rapid degradation during the first days of seed
CC germination.
CC -!- PTM: The C-terminal glycine may be removed from PA1B.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M13790; AAA33639.1; -.
CC EMBL; AJ276882; CAB82859.1; -.
CC InterPro; IPR011036; PH-related.
CC Plant toxin; Seed storage protein; Signal.
CC SIGNAL 1 26 Potential.
CC FT CHAIN 27 63 Albumin 1 B chain b.
CC FT PROPEP 64 69 Potential.
CC FT CHAIN 70 122 Albumin 1 B chain a.
CC FT PROPEP 123 130 Potential.
CC FT DISULFID 29 46 By similarity.
CC FT DISULFID 33 48 By similarity.
CC FT DISULFID 41 58 By similarity.
CC FT CONFLICT 10 10 M -> I (in Ref. 2).
CC FT CONFLICT 120 120 Q -> P (in Ref. 2).
CC SEQUENCE 130 AA; 13970 MW; F8B134A334490F5F CRC64;
SQ
Query Match 95.4%; Score 207; DB 1; Length 130;
Best Local Similarity 91.9%; Pred. No. 2.2e-16;
Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 ASCNGVCSPPFMPGCGSSACRCIPVGLVGYCRHPSG 37
|||||

```

```

Db 27 ASCNGVCSPPFMPGCGSSACRCIPVGLVGYCRHPSG 63

RESULT 6
Q6A1C7
ID Q6A1C7 PRELIMINARY; PRT; 96 AA.
AC Q6A1C7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative albumin 1 precursor (Fragment).
GN Name=pa1;
OS Vicia hirsuta.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3910;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Frisson; TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Delobel B.; Gressent F., Rahioui I., Dupont G., Diol O.,
RA Chessel D., Rahbe Y.;
RT "Broad screening of the legume family for variability of insecticidal
RT activities and occurrence of seed albumin 1b toxins.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784951; CAH05251.1; -.
KW SIGNAL.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 63 putative albumin 1b.
FT CHAIN 69 96 putative albumin 1a.
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10546 MW; DD8EF1B021A73DD7 CRC64;

Query Match 89.4%; Score 194; DB 2; Length 96;
Best Local Similarity 86.5%; Pred. No. 5.4e-15;
Matches 32; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 ASCNGVCSPPFMPGCGSSACRCIPVGLVGYCRHPSG 37
|||||
27 AECNGVCSPPFMPGCGSSACRCIPVGLVGYCRHPSG 63
|||||

AL1C_PEA
ID AL1C_PEA STANDARD; PRT; 130 AA.
AC P62928; P08687; Q04999; Q7XZC0; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 C precursor (PA1 C) [Contains: Albumin 1 C chain
DE b (PA1B C) (Leghemin C); Albumin 1 C chain a (PA1A C)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Frisson; TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
RN [2]
RP SEQUENCE OF 27-63, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC TISSUE=Seed;

```



```
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3848;
RN [1]
RN SEQUENCE FROM N.A.
RA Tan J.Z., Lou C.F., Hirano H.;
RA "Analysis of leguminin gene in soybean cultivar (Glycine max) and
RT wild species (Glycine soja).";
RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).
CC -1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity (By similarity).
CC -1- PFM: The C-terminal glycine may be removed from Alb.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ011935; CAA09880.2; -.
DR HSP; Q39837; 1J08.
KW Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1
FT CHAIN 20 56 Potential.
FT PROPEP 57 64 Albumin 1 chain b (By similarity).
FT CHAIN 65 117 Potential.
FT PROPEP 118 119 Albumin 1 chain a (Potential).
FT DISULFID 22 39 Potential.
FT DISULFID 26 41 By similarity.
FT DISULFID 34 51 By similarity.
FT SEQUENCE 119 AA; 12963 MW; EE5457D8D090700C CRC64;
SQ
Query Match 73.3%; Score 159; DB 1; Length 119;
Best Local Similarity 62.2%; Pred. No. 7.3e-11;
Matches 23; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 1 ASNCGVCSPPFEMPCCGTSAACRCIPVGLVIGYCRNPSSG 37
Db 20 ADCNGACSPFVPPPCRSSDCRCVPIGLVFGVCKIPTG 56
-----
RESULT 11
QYXZC5 PRELIMINARY; PRT; 140 AA.
AC Q7XZC5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Albumin 1 precursor.
GN Name=pal;
OS Medicago truncatula (Barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3880;
RN [1]
RN SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahloui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RA "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
DR EMBL; AJ574789; CAE00461.1; -.
DR HSP; Q39837; 1J08.
KW Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 140 albumin 1.
FT SEQUENCE 140 AA; 15426 MW; 519D9CEAB8924855 CRC64;
SQ
Query Match 71.9%; Score 156; DB 2; Length 140;
```

```
Best Local Similarity 73.5%; Pred. No. 1.8e-10;
Matches 25; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 3 CNGVCSPPFEMPCCGTSAACRCIPVGLVIGYCRNPSS 36
Db 30 CSGACSPFEMPCCRSDDCRCPVGLVAGYCTYPS 63
-----
RESULT 12
QYALD7 PRELIMINARY; PRT; 100 AA.
AC Q6ALD7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative albumin 1 precursor (Fragment).
GN Name=pal;
OS Astragalus monspessulanus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Galegeae; Astragalus.
OX NCBI_TaxID=287756;
RN [1]
RN SEQUENCE FROM N.A.
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]
RN SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahloui I., Duport G., Diol O.,
RA Chessel D., Rahbe Y.;
RT "Broad screening of the legume family for variability of insecticidal
RT activities and occurrence of seed albumin 1b toxins.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784941; CAH05241.1; -.
KW Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 64 putative albumin 1b.
FT CHAIN 73 >100 putative albumin 1a.
FT NON TER 100 100
FT SEQUENCE 100 AA; 10941 MW; 7CB8C76BD196587A CRC64;
SQ
Query Match 71.4%; Score 155; DB 2; Length 100;
Best Local Similarity 68.6%; Pred. No. 1.8e-10;
Matches 24; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 3 CNGVCSPPFEMPCCGTSAACRCIPVGLVIGYCRNPSSG 37
Db 30 CSGVCSPPFEMPCCGTSDCRCPVGLVFGVCKIPTG 64
-----
RESULT 13
ALBI_SOYBN STANDARD; PRT; 119 AA.
AC Q39837; O49854;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 precursor (Al) [Contains: Albumin 1 chain b (Alb)
DE (Leguminin); Albumin 1 chain a (Ala)].
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=cv. Miyagishiroe; TISSUE=Radicle;
RA MEDLINE=94357216; PubMed=8076636;
RA Watanabe Y., Barbaehov S.F., Komatsu S., Hemmings A.M., Miyagi M.,
RA Tsunashawa S., Hirano H.;
```


RT "A possible physiological function and the tertiary structure of a 4-
RL kDa peptide in legumes.";
CC Eur. J. Biochem. 270:1269-1276(2003).
CC -1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity (By similarity).
CC -1- PFM: The C-terminal glycine may be removed from Alb.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commerce/
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AB052881; BAB1938.1; --
DR HSP37; Q39837; 1J08.
KW Plant toxin; Seed storage protein; Signal.
FT NON TER 1 1
FT SIGNAL <1 1 Potential.
FT CHAIN 2 38 Albumin 1 chain b (By similarity).
FT PROPEP 39 46 Potential.
FT CHAIN 47 >89 Albumin 1 chain a (Potential).
FT DISULPID 4 21 By similarity.
FT DISULPID 8 23 By similarity.
FT DISULPID 16 33 By similarity.
FT NON TER 89 89
SQ SEQUENCE 89 AA; 9711 MW; 4ADEB9797083135B CRC64;

Query Match 70.5%; Score 153; DB 1; Length 89;
Best Local Similarity 64.9%; Pred. No. 2.9e-10;
Matches 24; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37
DB 2 ADNGAGSPFMPGCRSTDCRCIPALFGGFCINPTG 38

RESULT 16

ID Q6A1C9 PRELIMINARY; PRT; 98 AA.
AC Q6A1C9; (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Putative albumin 1 precursor (Fragment).
GN Name=pal;
OS Onobrychis viciifolia (Common sainfoin).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Hedyosarea; Onobrychis.
OX NCBI_TaxID=3882;
RN [1]
RP SEQUENCE FROM N.A.
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]

RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
RA Chessel D., Rabbe Y.;
RT "Broad screening of the legume family for variability of insecticidal
RT activities and occurrence of seed albumin lb toxins.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784949; CAH05249.1; --
KW Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 63 putative albumin 1b.
FT CHAIN 71 >98 putative albumin 1a.
FT NON TER 98 98
SQ SEQUENCE 98 AA; 10830 MW; 03072C77178A1E83 CRC64;

Query Match 70.5%; Score 153; DB 2; Length 98;
Best Local Similarity 65.7%; Pred. No. 3.1e-10;
Matches 23; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 SCNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNPS 36
DB 28 ACDGVCSPPFMPGCGTDCRCVPMGLFVGQCINPT 62

RESULT 17

Q6A1C8 PRELIMINARY; PRT; 99 AA.
AC Q6A1C8; (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Putative albumin 1 precursor (Fragment).
GN Name=pal;
OS Trigonella foenum-graecum (Fenugreek).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trigonella.
OX NCBI_TaxID=78534;
RN [1]
RP SEQUENCE FROM N.A.
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
RA Chessel D., Rabbe Y.;
RT "Broad screening of the legume family for variability of insecticidal
RT activities and occurrence of seed albumin lb toxins.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784950; CAH05250.1; --
KW Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 64 putative albumin 1b.
FT CHAIN 72 >99 putative albumin 1a.
FT NON TER 99 99
SQ SEQUENCE 99 AA; 10783 MW; 94D20EAD462018B4 CRC64;

Query Match 68.7%; Score 149; DB 2; Length 99;
Best Local Similarity 72.7%; Pred. No. .9e-10;
Matches 24; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 CNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 35
DB 30 CSGICSPFMPGCRSSDCRCIPVLVGGYCINP 62

RESULT 18

Q6A1D1 PRELIMINARY; PRT; 101 AA.
AC Q6A1D1; (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Putative albumin 1 precursor (Fragment).
GN Name=pal;
OS Mundulea sericea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Millettiae; Mundulea.
OX NCBI_TaxID=54460;
RN [1]
RP SEQUENCE FROM N.A.
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;

Search completed: March 28, 2005, 09:00:06
Job time : 87 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:50:15 ; Search time 23.5 Seconds
(without alignments)
151.490 Million cell updates/sec

Title: US-09-674-496D-6

Perfect score: 217

Sequence: 1 ASCNGVCSPPMPGCTGACRCIPVLGLVIGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 79:*

2: pir1:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	99.5	130	2 A25014	albumin precursor
2	154	71.0	119	2 S48192	insulin-like growth
3	73.5	33.9	1642	2 T19130	hypotheical prote
4	65	30.0	1104	2 T13869	transcription fact
5	62	28.6	1797	2 A55677	laminin beta-2 cha
6	60	27.6	61	1 SMBO2	metallothionein II
7	60	27.6	61	2 S00808	metallothionein Ia
8	60	27.6	61	2 S00810	metallothionein Ib
9	60	27.6	61	2 S00809	laminin beta-2 cha
10	58	26.7	1801	1 MWRYS	cathepsin B-like c
11	57	26.3	174	2 B48454	testis-specific pr
12	56	25.8	56	1 WTF	metallothionein I
13	56	25.8	61	2 A23889	metallothionein 1
14	56	25.8	270	2 F71699	diaminopimelate ep
15	56	25.8	375	2 T16248	hypotheical prote
16	56	25.8	452	2 T13983	angio-associated m
17	56	25.8	813	2 T21192	hypotheical prote
18	55	25.3	61	2 T148173	metallothionein II
19	55	25.3	1798	2 S53869	laminin beta-2 cha
20	55	25.3	2437	2 S42612	transmembrane prot
21	55	25.3	3075	2 S14458	laminin alpha-1 ch
22	54.5	25.1	1574	2 T13954	MEGF6 protein - ra
23	53.5	24.7	85	2 T05719	metallothionein II
24	53.5	24.7	87	2 F88369	small cysteine-ric
25	53.5	24.7	1160	2 C88369	protein unc-52 [im
26	53.5	24.7	2295	2 C88369	protein unc-52 [im
27	53.5	24.7	3375	2 T19821	hypotheical prote
28	53	24.4	61	1 SMMS2	metallothionein II
29	53	24.4	61	2 T157572	metallothionein II

30	53	24.4	450	2	T17234	hypotheical prote
31	52	24.0	61	1	SMH2C	metallothionein II
32	52	24.0	61	2	S18403	metallothionein II
33	52	24.0	61	2	T48116	testis-specific pr
34	52	24.0	74	2	S25773	testis-specific pr
35	52	24.0	274	2	F64090	diaminopimelate ep
36	52	24.0	336	2	S33879	plasma precursor
37	52	24.0	408	1	QRHUB	beta-3-adrenergic
38	52	24.0	414	1	QRHUB3	beta-3-adrenergic
39	51.5	23.7	861	2	B49847	nitrate reductase
40	51.5	23.7	1786	1	MMHUB1	laminin beta-1 cha
41	51.5	23.7	4544	1	S02392	alpha-2-macroglobu
42	51.5	23.7	4545	1	S25111	alpha-2-macroglobu
43	51.5	23.7	6420	2	T30283	polyketide synthase
44	51	23.5	61	1	SMRT2	metallothionein II
45	51	23.5	151	2	S60314	hair keratin cyste
46	51	23.5	281	1	ZBBE12	30.2K zinc-binding
47	51	23.5	322	2	T27966	hypotheical prote
48	51	23.5	457	2	T46332	hypotheical prote
49	51	23.5	473	2	A56175	adhesive plaque pr
50	51	23.5	706	2	A48084	STELL protein kina
51	51	23.5	856	1	A44963	env polyprotein pr
52	51	23.5	1131	2	T38744	hypotheical prote
53	51	23.5	1364	2	T00250	MEGF2 protein - hu
54	51	23.5	3084	1	MMMSA	laminin alpha-1 ch
55	50.5	23.3	160	2	T25185	hypotheical prote
56	50.5	23.3	290	2	T21185	hypotheical prote
57	50.5	23.3	309	2	T28708	hypotheical prote
58	50.5	23.3	379	2	A59180	Wnt inhibitory fac
59	50.5	23.3	1101	2	T16840	hypotheical prote
60	50.5	23.3	1888	2	D86236	protein F14N23.5 l
61	50.5	23.3	1808	2	T15099	hypotheical prote
62	50	23.0	61	1	SMHUIG	metallothionein I
63	50	23.0	61	1	SMH1C	metallothionein I
64	50	23.0	270	2	C97772	diaminopimelate ep
65	50	23.0	316	2	T33776	hypotheical prote
66	50	23.0	342	2	A48454	cathepsin B-like c
67	50	23.0	579	2	JC7629	membrane-type friz
68	50	23.0	915	1	A55144	autotaxin precursor
69	49.5	22.8	160	2	S28290	hypotheical prote
70	49.5	22.8	228	2	S45677	proteinase inhibit
71	49.5	22.8	245	1	A47539	homeotic protein g
72	49.5	22.8	372	2	T29359	hypotheical prote
73	49.5	22.8	400	2	S32804	beta-3-adrenergic
74	49.5	22.8	480	2	AF3057	glycogen synthase
75	49.5	22.8	480	2	H98228	p-selectin precurs
76	49.5	22.8	768	2	A42755	hypotheical prote
77	49.5	22.8	787	2	PN0677	hypotheical prote
78	49.5	22.8	1006	2	JC5526	kinase-defective E
79	49	22.6	55	2	S25774	testis-specific pr
80	49	22.6	61	1	SMHUIE	metallothionein I
81	49	22.6	61	1	SMHUIF	metallothionein 1F
82	49	22.6	61	1	SMHUI2	metallothionein 2
83	49	22.6	61	1	SMHUI1	metallothionein 1
84	49	22.6	61	1	SMHUI2	metallothionein 2
85	49	22.6	61	1	SMHUI1	metallothionein 1
86	49	22.6	61	1	SMRT1	metallothionein 1
87	49	22.6	61	2	I54574	metallothionein-1
88	49	22.6	61	2	S47652	metallothionein 1X
89	49	22.6	61	2	B23889	metallothionein 1
90	49	22.6	61	2	S00811	metallothionein 2
91	49	22.6	108	2	S43154	diaminopimelate ep
92	49	22.6	145	2	T15608	hypotheical prote
93	49	22.6	214	2	S15326	fimbrial protein M
94	49	22.6	214	2	T32177	hypotheical prote
95	49	22.6	276	2	G82986	diaminopimelate ep
96	49	22.6	277	2	I52825	gene MAC25 protein
97	49	22.6	282	2	S50031	prostaglandin-simu
98	49	22.6	334	2	A48151	sperm tail protein
99	49	22.6	335	2	T31730	hypotheical prote
100	49	22.6	348	2	B48435	cysteine proteinase

ALIGNMENTS

RESULT 1

A25014
albumin precursor - garden pea
C/Species: Pisum sativum (garden pea)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C/Accession: A25014
R/Higgins, T.J.V.; Chandler, P.M.; Randall, P.J.; Spencer, D.; Beach, L.R.; Blagrove, R.
J. Biol. Chem. 261, 11124-11130, 1986
A/Title: Gene structure, protein structure, and regulation of the synthesis of a sulfur-
A/Reference number: A25014; MUID:86278210; PMID:3755437
A/Accession: A25014
A/Molecule type: DNA
A/Residues: 1-130 <HIG>
A/Cross-references: UNIPROT:P08687; GB:M13709; NID:g169024; PIDN:AAA33638.1; PID:g169025
C/Genetics:
A/Introns: 17/1
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-130/Product: albumin #status predicted <MAT>

Query Match 99.5%; Score 216; DB 2; Length 130;
Best Local Similarity 97.3%; Pred. No. 1.6e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37
|||||
Db 27 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 63
|||||

RESULT 2

S48192
insulin-like growth factor S11 precursor - soybean
N/Alternate names: leguminin
C/Species: Glycine max (soybean)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S48192
R/Watanabe, Y.; Barbashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunasawa, S.;
Eur. J. Biochem. 224, 167-172, 1994
A/Title: A peptide that stimulates phosphorylation of the plant insulin-binding protein.
A/Reference number: S48192; MUID:94357216; PMID:8076638
A/Accession: S48192
A/Molecule type: mRNA; protein
A/Residues: 1-119 <MAT>
A/Cross-references: UNIPROT:Q39837; GB:D17396; NID:g498167; PIDN:BAA04219.1; PID:g498168
R/Barbashov, S.F.; Egorov, T.A.
Mol. Biol. (Mosk.) 24, 953-961, 1990
A/Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cell g
A/Reference number: PN0115; MUID:91066897; PMID:2250683
A/Accession: PN0116
A/Molecule type: protein
A/Residues: 20-30; M, 33-39 <BAR>
F;1-19/Domain: propeptide #status predicted <PRO>
F;20-56/Product: insulin-like growth factor S11 #status experimental <MAT>

Query Match 71.0%; Score 154; DB 2; Length 119;
Best Local Similarity 59.5%; Pred. No. 1.4e-10;
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37
|||||
Db 20 ADCNGACSPFVPPCRSDRCRVPGLFVGFCIHPTG 56
|||||

RESULT 3

T19130
hypothetical protein C09F9.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T19130
R/Smye, R.
submitted to the EMBL Data Library, November 1996

A/Reference number: Z19078

A/Accession: T19130
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1642 <WIL>

A/Cross-references: UNIPROT:O62055; EMBL:Z81465; PIDN:CA803861.1; GSPDB:GN000020; CESP:CO;

A/Experimental source: clone C09F9

C/Genetics:

A/Gene: CESP:C09F9.2

A/Map position: 2

A/Introns: 75/3; 103/2; 220/1; 552/1; 1500/3; 1517/1; 1578/3

Query Match 33.9%; Score 73.5; DB 2; Length 1642;
Best Local Similarity 37.8%; Pred. No. 1.12;
Matches 14; Conservative 5; Mismatches 13; Indels 5; Gaps 1;

QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37
|||||
Db 509 ADCFSIFTRSECTDCGSAACACLIQ-----GYARNPQG 540
|||||

RESULT 4

I38869
transcription factor NFX1 [imported] - human
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: I38869
R/Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.
J. Exp. Med. 180, 1763-1774, 1994
A/Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the
n and functions as a transcriptional repressor.
A/Reference number: I38869; MUID:95053707; PMID:7964459
A/Accession: I38869
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1104 <RES>

A/Cross-references: UNIPROT:Q12986; EMBL:U15306; NID:g563216; PIDN:AAA69517.1; PID:g56321

F;338-398/Domain: RING finger homology <RRN>

Query Match 30.0%; Score 65; DB 2; Length 1104;
Best Local Similarity 34.1%; Pred. No. 8;
Matches 15; Conservative 4; Mismatches 15; Indels 10; Gaps 3;

QY 2 SCNGVCSPPFMPGCG---TSACRC-----IPVGLVIG-YCRNP 35
|||||
Db 440 SCNLLCHPGCPCPAFMTKTCGGRTRTVRCGQAVSVHCNP 483
|||||

RESULT 5

A55677
laminin beta-2 chain precursor (version 1) - human
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C/Accession: A55677
R/Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliand, M.F.;
Genomics 24, 243-252, 1994
A/Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
A/Reference number: A55677; MUID:95213013; PMID:7698745
A/Accession: A55677
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1797 <WEW>
A/Cross-references: GB:X79683
C/Genetics:
A/Gene: GDB:LAMB2

A/Cross-references: GDB:132363; OMIM:150325

A/Map position: 3p21.3-3p21.2

C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C/Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer

F;1-32/Domain: signal sequence #status predicted <SIG>

F;33-1797/Product: laminin beta-2 chain #status predicted <MAT>

F;283-344/Domain: laminin-type EGF-like homology <LE01>

F;347-407/Domain: laminin-type EGF-like homology <LE02>

F:410-467/Domain: laminin-type EGF-like homology <LE03>
F:470-539/Domain: laminin-type EGF-like homology <LE04>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:783-828/Domain: laminin-type EGF-like homology <LE06>
F:831-874/Domain: laminin-type EGF-like homology <LE07>
F:877-924/Domain: laminin-type EGF-like homology <LE08>
F:927-962/Domain: laminin-type EGF-like homology <LE09>
F:985-1034/Domain: laminin-type EGF-like homology <LE10>
F:1037-1091/Domain: laminin-type EGF-like homology <LE11>
F:1094-1139/Domain: laminin-type EGF-like homology <LE12>
F:1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 28.6%; Score 62; DB 2; Length 1797;
Best Local Similarity 36.4%; Pred. No. 25;
Matches 12; Conservative 4; Mismatches 15; Indels 2; Gaps 1;

Qy 7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSSG 37
Db 816 CAPGYGFGPTGCQCQCSPRGALSSLCRTSG 848

RESULT 6
SMBO2
metallothionein II - bovine
N:Alternate names: MT-II
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A03279
R:Winge, D.R.; Gray, W.R.; Zelazowski, A.; Garvey, J.S.
Arch. Biochem. Biophys. 245, 254-262, 1986
A:Title: Sequence and antigenicity of calf metallothionein II.
A:Reference number: A03279; UID:86129456; PMID:3947100
A:Accession: A03279
A:Molecule type: protein
A:Residues: 1-61 <WIN>
A:Cross-references: UNIPROT:P04356
A:Experimental source: calf liver
A:Comment: 49-ile was also found
C:Note: The vertebrate metallothioneins contain two metal-binding domains. Clusters c
C:Comment: Cysteine clusters can also chelate univalent metal ions. As many as 18 differ
C:Superfamily: metallothionein
C:Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster
F:1-29/Domain: beta <NH2>
F:30-61/Domain: alpha <AUP>
F:1/Modified site: acetylated amino end (Met) #status experimental
F:5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F:33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre

Query Match 27.6%; Score 60; DB 1; Length 61;
Best Local Similarity 44.4%; Pred. No. 3.3;
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

Qy 2 SCNG--VCSPPFMPGCGTSACRCIPVG 26
Db 14 SCAGSCTKACRCPCSKKSCCSCCPVG 40

RESULT 7
S00808
metallothionein Ia - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S00808; I46414; I46559
R:Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
Eur. J. Biochem. 174, 417-424, 1988
A:Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel
A:Reference number: S00808; UID:86254812; PMID:3383853
A:Accession: S00808
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-61 <PET>
A:Cross-references: UNIPROT:P04356; GB:X04626; NID:g4218467; PIDN:CAA28299.1; PID:g42184
R:Peterson, M.G.; Mercer, J.F.

Eur. J. Biochem. 160, 579-585, 1986
A:Title: Structure and regulation of the sheep metallothionein-Ia gene.
A:Reference number: I46414; UID:87053978; PMID:3780723
A:Accession: I46414
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-49, 'S', 51-61 <PET2>
A:Cross-references: EMBL:X04626; NID:g4218467
R:Peterson, M.G.; Lazdins, I.; Danks, D.M.; Mercer, J.F.
Eur. J. Biochem. 143, 507-511, 1984
A:Title: Cloning and sequencing of a sheep metallothionein cDNA.
A:Reference number: I46559; UID:85003624; PMID:6434305
A:Accession: I46559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-61 <PET3>
A:Cross-references: EMBL:X00953; NID:g1825; PIDN:CAA25464.1; PID:g1826
C:Genetics:
A:Introns: 10/1; 32/1
C:Superfamily: metallothionein

Query Match 27.6%; Score 60; DB 2; Length 61;
Best Local Similarity 44.4%; Pred. No. 3.3;
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

Qy 2 SCNG--VCSPPFMPGCGTSACRCIPVG 26
Db 14 SCAGSCTKACRCPCSKKSCCSCCPVG 40

RESULT 8
S00810
metallothionein Ic - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S00810
R:Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
Eur. J. Biochem. 174, 417-424, 1988
A:Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel
A:Reference number: S00808; UID:86254812; PMID:3383853
A:Accession: S00810
A:Molecule type: DNA
A:Residues: 1-61 <PET>
A:Cross-references: UNIPROT:P09578; EMBL:X07974; NID:g1340; PIDN:CAA30786.1; PID:g1341
C:Genetics:
A:Introns: 10/1; 32/1
C:Superfamily: metallothionein

Query Match 27.6%; Score 60; DB 2; Length 61;
Best Local Similarity 44.4%; Pred. No. 3.3;
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

Qy 2 SCNG--VCSPPFMPGCGTSACRCIPVG 26
Db 14 SCAGSCTKACRCPCSKKSCCSCCPVG 40

RESULT 9
S00809
metallothionein Ib - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S00809
R:Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
Eur. J. Biochem. 174, 417-424, 1988
A:Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel
A:Reference number: S00808; UID:86254812; PMID:3383853
A:Accession: S00809
A:Molecule type: DNA
A:Residues: 1-61 <PET>
A:Cross-references: UNIPROT:P09577; EMBL:X07973; NID:g1338; PIDN:CAA30785.1; PID:g1339
C:Genetics:
A:Introns: 10/1; 32/1

C;Superfamily: metallothionein

Query Match 27.6%; Score 60; DB 2; Length 61;
Best Local Similarity 44.4%; Pred. No. 3.3;
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

QY 2 SCNG--VCSFPEPMPGCTSCRCIPVG 26
|||
Db 14 SCAGSTCKACRCFCSCCKSCCPCVG 40

RESULT 10

NR15
laminin beta-2 chain precursor - rat
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
A;Reference number: S03539; MUID:89159410; PMID:2922051
A;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sances, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro
C;Keywords: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
A;Accession: S03539

A;Molecule type: mRNA
A;Residues: 1-1801 <HUN>
A;Cross-references: UNIPROT:P15800; EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F;36-285/Domain: VI <DOM6>
F;286-555/Domain: V <DOM5>
F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;473-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;556-784/Domain: IV <DOM4>
F;786-831/Domain: laminin-type EGF-like homology <LE06>
F;788-1196/Domain: III <DOM3>
F;834-877/Domain: laminin-type EGF-like homology <LE07>
F;880-927/Domain: laminin-type EGF-like homology <LE08>
F;930-986/Domain: laminin-type EGF-like homology <LE09>
F;989-1038/Domain: laminin-type EGF-like homology <LE10>
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I <DOM1>
F;45-50/Diulfide bonds: #status predicted
F;251,371,1098,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F;1193,1196,1800/Diulfide bonds: interchain #status predicted

Query Match 26.7%; Score 58; DB 1; Length 1801;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 14 PGTSACRCIPVGLVIGYCRNPSG 37
|||
Db 828 PAGCQACQSPDGAUSALCEGTSG 851

RESULT 11

B48454
cathepsin B-like cysteine proteinase (EC 3.4.22.1) CP-3 - nematode (Ostertagia ostertagi)
C;Species: Ostertagia ostertagi
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: B48454
R;Pratt, D.; Boisvenue, R.J.; Cox, G.N.
Mol. Biochem. Parasitol. 56, 39-48, 1992
A;Title: Isolation of putative cysteine protease genes of Ostertagia ostertagi.
A;Reference number: A48454; MUID:93116804; PMID:11475000
A;Accession: B48454
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <PRA>
A;Cross-references: UNIPROT:Q06544; GB:M88505; NID:g159951; PIDN:AAA29436.1; PID:g159952
A;Experimental source: larva
A;Note: sequence extracted from NCBI backbone (NCBIN:121411, NCBI:P:124017)
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase; protein degradation

Query Match 26.3%; Score 57; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GVCSPFEMPCCG 16
|||
Db 20 GCRPVERPCCG 31

RESULT 12

WTF
testis-specific protein (clone mat(3)gl-9) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00340
R;Kuhn, R.; Schaefer, U.; Schaefer, M.
EMBO J. 7, 447-454, 1988
A;Title: Cis-acting regions sufficient for spermatocyte-specific transcriptional and spe
A;Reference number: S00340; MUID:88211557; PMID:2835228
A;Accession: S00340
A;Molecule type: DNA
A;Residues: 1-56 <KUH>
A;Cross-references: UNIPROT:P08175; EMBL:Y00831; NID:g8650; PIDN:CAA68761.1; PID:g8651
C;Genetics:
A;Gene: FlyBase:Mat87F
A;Cross-references: FlyBase:FBgn0002862
C;Superfamily: fruit fly testis-specific protein
C;Keywords: sex-specific protein; testis

Query Match 25.8%; Score 56; DB 1; Length 56;
Best Local Similarity 38.2%; Pred. No. 8.7;
Matches 13; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

QY 3 CNGVCSPFEMPCCGTSACRCIPVGLVIGYCRNPS 36
|||
Db 2 CCGPCGPGCCGCGCCGCGCGCGPCYGN 35

RESULT 13

A23889
metallothionein 1 - bovine (tentative sequence)
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23889
R;Munger, K.; Germann, U.A.; Beltramini, M.; Niedermann, D.; Baitella-Eberle, G.; Kagi, J. Biol. Chem. 260, 10032-10038, 1985
A;Title: (Cu,Zn)-metallothioneins from fetal bovine liver. Chemical and spectroscopic pr
A;Reference number: A92490; MUID:85261416; PMID:4019500
A;Accession: A23889
A;Molecule type: protein
A;Residues: 1-61 <MUN>
A;Cross-references: UNIPROT:P58280
C;Superfamily: metallothionein

Query Match 25.8%; Score 56; DB 2; Length 61;
Best Local Similarity 44.0%; Pred. No. 9.3;
Matches 11; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

Qy 2 SCNGVCSPPFEMPCCGTSAACRCIPVG 26
Db 18 SK--CKACRCPSCKKSCCSCPVG 40

RESULT 14
F71699
diaminopimelate epimerase (dapF) RP415 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: F71699
R:Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alemark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: F71699
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-270 <AND>
A:Cross-references: UNIPROT:Q9ZDB7; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA1487
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: dapF; RP415
C:Superfamily: diaminopimelate epimerase

Query Match 25.8%; Score 56; DB 2; Length 270;
Best Local Similarity 40.9%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 15 CGTSACRCIPVGLVIGYCRNPS 36
Db 213 CGSGACASFAAGLKLGVHSPS 234

RESULT 15
T16248
hypothetical protein F35A5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16248
R:Leimbach, D.
submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid F35A5.
A:Reference number: Z18485
A:Accession: T16248
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-375 <LEI>
A:Cross-references: UNIPROT:Q20002; EMBL:U46675; NID:g1166613; PID:g1166616; PIDN:AAB526
A:Experimental source: strain Bristol N2; clone F35A5
C:Genetics:
A:Gene: CESP:F35A5.3
A:Map position: X
A:Introns: 14/3; 128/3; 187/3; 216/3; 246/3; 284/3
C:Superfamily: gliadin

Query Match 25.8%; Score 56; DB 2; Length 375;
Best Local Similarity 36.7%; Pred. No. 37;
Matches 11; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

Qy 2 SCNGVCSPPFEMPCCGTSAACRCIPV 25
Db 73 ACN--CAPVQDPCACOPQQQPCACNAPV 100

RESULT 16
I39383
angio-associated migratory cell protein - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004
C:Accession: I39383
R:Beckner, W.E.; Kruttsch, H.C.; Stracke, M.L.; Williams, S.T.; Gallardo, J.A.; Liotta, Cancer Res. 55, 2140-2149, 1995

A:Title: Identification of a new immunoglobulin superfamily protein expressed in blood vessels
A:Reference number: I39383; MUID:95262124; PMID:7743515
A:Accession: I39383
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-452 <RES>
A:Cross-references: UNIPROT:Q13685; GB:M95627; NID:g870802; PIDN:AAA68889.1; PID:g870803
C:Genetics:
A:Gene: GDB:AAMP
A:Cross-references: GDB:4573993
A:Map position: 14q32.1-14q32.1
C:Superfamily: WD repeat homology
F:148-181/Domain: WD repeat homology <WD1>
F:414-447/Domain: WD repeat homology <WD2>

Query Match 25.8%; Score 56; DB 2; Length 452;
Best Local Similarity 40.0%; Pred. No. 42;
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

Qy 4 NGVCSPFEMPCCGTSAACRCIPVG--LVIGY 31
Db 223 NGDKCTFGPNCPCATCGRVLPDGKRAVVG 252

RESULT 17
T21192
hypothetical protein F21C3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21192
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19388
A:Accession: T21192
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-813 <WIL>
A:Cross-references: UNIPROT:Q19673; EMBL:Z71261; PIDN:CAA95805.1; GSPDB:GN00019; CESP:F2
A:Experimental source: clone F21C3
C:Genetics:
A:Gene: CESP:F21C3.2
A:Map position: 1
A:Introns: 39/1; 105/3; 175/3; 220/1; 294/3; 320/2; 345/3; 386/3; 443/3; 508/2; 635/1; 6

Query Match 25.8%; Score 56; DB 2; Length 813;
Best Local Similarity 26.3%; Pred. No. 65;
Matches 15; Conservative 7; Mismatches 15; Indels 20; Gaps 3;

Qy 1 ASCNG-----VCSPFEMP-----PCGTSAC-----RCIPVGLVIGYCRNPSG 37
Db 676 ATCGGGGGADSGISNPTTTPATNNGQNTPCDSPMCYNEDQCCPIWAQRGQCRSNPG 732

RESULT 18
I48173
metallothionein II - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48173
R:Duguid, J.R.; Rohwer, R.G.; Seed, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 5738-5742, 1988
A:Title: Isolation of cDNAs of scrapie-modulated RNAs by subtractive hybridization of a
A:Reference number: I48171; MUID:88289792; PMID:2456562
A:Accession: I48173
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-61 <RES>
A:Cross-references: UNIPROT:P17808; GB:J03848; NID:g191448; PIDN:AAA37101.1; PID:g305363
C:Superfamily: metallothionein

Query Match 25.3%; Score 55; DB 2; Length 61;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 12; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

—

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 09:00:16 ; Search time 68.5 Seconds
(without alignments)
178.843 Million cell updates/sec

Title: US-09-674-496d-6

Perfect score: 217

Sequence: 1 ASNGVCSPEMPGCTGACRCIPVGLVIGVCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	73.3	127	15	US-10-424-599-167170
2	101	46.5	80	15	US-10-424-599-210838
3	88	40.6	18	11	US-09-782-130-12
4	86	39.6	101	15	US-10-424-599-269230
5	75	34.6	18	11	US-09-782-130-17
6	65	30.0	1024	16	US-10-408-765A-1481
7	65	30.0	1728	14	US-10-184-644-313
8	65	30.0	1728	14	US-10-184-634-313
9	65	30.0	1728	14	US-10-063-685-101
10	62	28.6	1798	9	US-09-845-583-8
11	60.5	27.9	2692	14	US-10-184-644-225
12	60.5	27.9	2692	14	US-10-184-634-225
13	60	27.6	1871	14	US-10-184-644-301

60	27.6	1871	14	US-10-184-634-301	Sequence 301, App
60	27.6	1871	14	US-10-063-685-91	Sequence 91, Appl
59.5	27.4	1355	14	US-10-123-155-421	Sequence 421, App
59.5	27.4	1355	14	US-10-146-731-421	Sequence 421, App
59.5	27.4	1355	14	US-10-140-472-421	Sequence 421, App
59.5	27.4	1355	14	US-10-141-761-421	Sequence 421, App
59.5	27.4	1355	14	US-10-142-885-421	Sequence 421, App
59.5	27.4	1355	14	US-10-158-790-421	Sequence 421, App
59.5	27.4	1355	15	US-10-137-871-421	Sequence 421, App
59.5	27.4	1355	15	US-10-140-923-421	Sequence 421, App
59.5	27.4	1355	15	US-10-141-756-421	Sequence 421, App
59.5	27.4	1355	15	US-10-141-759-421	Sequence 421, App
59.5	27.4	1355	15	US-10-140-805-421	Sequence 421, App
59.5	27.4	1355	15	US-10-140-864-421	Sequence 421, App
59.5	27.4	1355	15	US-10-142-426-421	Sequence 421, App
59	27.2	975	9	US-09-886-055-431	Sequence 431, App
59	27.2	1799	9	US-09-845-583-6	Sequence 6, Appli
58.5	27.0	1101	15	US-10-287-971-18	Sequence 18, Appl
58.5	27.0	1102	14	US-10-073-912-11	Sequence 11, Appl
58.5	27.0	3004	14	US-10-184-644-91	Sequence 91, Appl
58.5	27.0	3004	14	US-10-184-634-91	Sequence 91, Appl
58.5	27.0	3690	14	US-10-184-644-517	Sequence 517, App
58.5	27.0	3690	14	US-10-184-634-517	Sequence 517, App
58	26.7	413	13	US-10-087-192-519	Sequence 519, App
58	26.7	1801	9	US-09-938-275-8	Sequence 8, Appli
57.5	26.5	84	15	US-10-424-599-201814	Sequence 201814,
57.5	26.5	85	16	US-10-437-963-161069	Sequence 161069,
57.5	26.5	581	10	US-09-244-805-27	Sequence 27, Appl
57.5	26.5	581	10	US-09-245-277-27	Sequence 27, Appl
57.5	26.5	581	16	US-10-792-481-27	Sequence 28, Appl
57.5	26.5	7285	14	US-10-145-206-28	Sequence 40, Appl
57	26.3	67	14	US-10-087-887-40	Sequence 40, Appl
57	26.3	67	15	US-10-038-854-185	Sequence 185, App
57	26.3	101	15	US-10-424-599-158972	Sequence 158972,
57	26.3	101	15	US-10-425-114-49681	Sequence 49681, A
56.5	26.0	517	15	US-10-425-114-38947	Sequence 38947, A
56.5	26.0	682	15	US-10-424-599-283322	Sequence 285322,
56	25.8	100	15	US-10-424-599-193634	Sequence 193634,
56	25.8	141	9	US-09-764-864-1489	Sequence 1489, Ap
56	25.8	371	16	US-10-437-963-146358	Sequence 146358,
56	25.8	452	16	US-10-789-378-2	Sequence 2, Appli
56	25.8	452	17	US-10-868-578A-24	Sequence 24, Appl
56	25.8	611	10	US-09-893-519A-28	Sequence 28, Appl
55.5	25.6	92	14	US-10-072-602B-219	Sequence 219, App
55.5	25.6	179	14	US-10-017-161-1510	Sequence 1510, Ap
55.5	25.6	708	14	US-10-184-644-211	Sequence 211, App
55.5	25.6	708	14	US-10-184-634-211	Sequence 211, App
55.5	25.6	1034	15	US-10-052-648A-31	Sequence 31, Appl
55.5	25.6	1034	15	US-10-052-648A-32	Sequence 32, Appl
55.5	25.6	1331	16	US-10-437-963-193234	Sequence 193234,
55.5	25.6	1730	14	US-10-123-155-7	Sequence 7, Appli
55.5	25.6	1730	14	US-10-146-731-7	Sequence 7, Appli
55.5	25.6	1730	14	US-10-140-472-7	Sequence 7, Appli
55.5	25.6	1730	14	US-10-141-761-7	Sequence 7, Appli
55.5	25.6	1730	14	US-10-142-885-7	Sequence 7, Appli
55.5	25.6	1730	14	US-10-158-790-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-137-871-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-140-923-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-141-756-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-141-759-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-140-805-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-140-864-7	Sequence 7, Appli
55.5	25.6	1730	15	US-10-142-426-7	Sequence 7, Appli
55	25.3	143	16	US-10-437-963-167377	Sequence 167377,
55	25.3	162	9	US-09-864-761-34582	Sequence 34582, A
55	25.3	301	16	US-10-437-963-167378	Sequence 167378,
55	25.3	364	16	US-10-437-963-139584	Sequence 139584,
55	25.3	377	16	US-10-437-963-154620	Sequence 154620,
55	25.3	397	16	US-10-437-963-154624	Sequence 154624,
55	25.3	691	16	US-10-437-963-119124	Sequence 119124,
55	25.3	1543	15	US-10-072-012-320	Sequence 320, App
55	25.3	1798	9	US-09-938-275-9	Sequence 9, Appli
55	25.3	2478	14	US-10-063-685-163	Sequence 163, App

Sequence 5, Appli
Sequence 191209,
Sequence 4, Appli
Sequence 271846,
Sequence 77, Appl
Sequence 283, App
Sequence 3966, Ap
Sequence 29453, A
Sequence 4652, Ap
Sequence 161876,
Sequence 160854,
Sequence 172038,
Sequence 269, App
Sequence 269, App

ALIGNMENTS

RESULT 1
US-10-424-599-167170
; Sequence 167170, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167170
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_121970C.1.pap
US-10-424-599-167170

Query Match 73.3%; Score 159; DB 15; Length 127;
Best Local Similarity 64.9%; Pred. No. 1.3e-09;
Matches 24; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ASCNGVSPPEMPCGTSAACRCIPVGLVIGYCRNP 37
Db 28 ADCNGACSPPEMPCRSRDCRVPGLVAGFCIHPTG 64

RESULT 2
US-10-424-599-210838
; Sequence 210838, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210838
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(80)

; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32413C.1.pap
US-10-424-599-210838
Query Match 46.5%; Score 101; DB 15; Length 80;
Best Local Similarity 43.2%; Pred. No. 0.0013;
Matches 16; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ASCNGVSPPEMPCGTSAACRCIPVGLVIGYCRNP 37
Db 28 ADCIGCTSFYIPCLSRDCRSVIXLITGFCIHPSG 64

RESULT 3
US-09-782-130-12
; Sequence 12, Application US/09782130
; Publication No. US20040055038A1
; GENERAL INFORMATION:
; APPLICANT: KNAUF, VIC C.
; APPLICANT: KRIDL, JEAN C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION
; TITLE OF INVENTION: AND EXPRESSION OF HETEROLOGOUS GENES
; FILE REFERENCE: 16518.052
; CURRENT APPLICATION NUMBER: US/09/782,130
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/232,861
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 08/812,665
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 08/484,941
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/105,852
; PRIOR FILING DATE: 1993-08-10
; PRIOR APPLICATION NUMBER: US 07/526,123
; PRIOR FILING DATE: 1990-05-21
; PRIOR APPLICATION NUMBER: US 07/267,685
; PRIOR FILING DATE: 1988-11-02
; PRIOR APPLICATION NUMBER: US 06/692,605
; PRIOR FILING DATE: 1985-01-17
; PRIOR APPLICATION NUMBER: US 07/582,241
; PRIOR FILING DATE: 1990-09-14
; PRIOR APPLICATION NUMBER: US 07/188,361
; PRIOR FILING DATE: 1988-04-29
; PRIOR APPLICATION NUMBER: US 07/168,190
; PRIOR FILING DATE: 1988-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protease
; OTHER INFORMATION: Inhibitor PALB peptide sequence
US-09-782-130-12

Query Match 40.6%; Score 88; DB 11; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.0092;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VCSFPEMPCGTSAACRCI 23
Db 1 VCSFFDIPCGSPLCRCI 18

RESULT 4
US-10-424-599-269230
; Sequence 269230, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

Query Match 30.0%; Score 65; DB 14; Length 1728;
Best Local Similarity 34.4%; Pred. No. 1.2e+02;
Matches 11; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ASCNGVCSFFEMPPOGTSACRIPVGLVGYC 32
| | | | | | | | | | | | | | | | | | | | | |
Db 1191 ACCGGACAGAGTGTCATTCACCTTGCAAGTC 1222
| | | | | | | | | | | | | | | | | | | | | |

```

RESULT 8
US-10-184-634-313
; Sequence 313, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C1217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 313
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-313

```

Query Match 30.0%; Score 65; DB 14; Length 1728;
Best Local Similarity 34.4%; Pred. NO. 1.2e+02;
Matches 11; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ASCNGVCSFFEMPFGTSACRCIPVGLVIGYC 32
| | | | | : | | | | |
Db 1191 ACCGGACAGAGTGTCAATCCACCTTGCAAGTC 1222

```

RESULT 9
US-10-063-685-101
; Sequence 101, Application US/10063685
; Publication No. US20030180909A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,685
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 101
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-685-101

```

Query Match 30.0%; Score 65; DB 14; Length 1728;
Best Local Similarity 34.4%; Pred. No. 1.2e+02;
Matches 11; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ASCNGVCSFFEMPPCGTSAACRCIPVGLVIGYC 32
| | | | | | | | | | | | | | | | | | | | | |
Db 1191 ACCGGACAGAGTGTCATTCCACCTTGAAGTC 1222

```

RESULT 10
US-09-845-583-8
; Sequence 8, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-583-8

```

Query Match 28.6%; Score 62; DB 9; Length 1798;
Best Local Similarity 36.4%; Pred. No. 2.7e+02;
Matches 12; Conservative 4; Mismatches 15; Indels 2; Gaps 1;

Qy	7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37
	: : : : : : :
Db	816 CAPGYGFPTGCQACQCSPRGALSSLCERTSG 848

```

RESULT 11
US-10-184-644-225
; Sequence 225, Application US/10184644
; Publication No. US2003004930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT Filing DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 225
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-225

Query Match          27.9%; Score 60.5; DB 14; Length 2692;
Best Local Similarity 37.5%; Pred. No. 5.5e+02;

```

Matches 12; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

QY 1 ASCNGVCSPPFMPGCGTSACRCIPVGLVIGYC 32
| | | | |
| : | | | | |
Db 350 ATCGGGCCGTGGCGCTCGTTTCTCAATG---GCC 378

RESULT 12

```

US-10-184-634-225
; Sequence 225, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 225
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-225

```

Query Match 27.9%; Score 60.5; DB 14; Length 2692;

Best Local Similarity 37.5%; Pred. No. 5.5e+02;
Matches 12; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

Qy 1 ASCNGVCSPFEMPPCGTSAACRCPVGLVIGYC 32
Db 350 ATCGGCCGTGGCCTCGTTTCTCAATG---GCC 378

RESULT 13

```

US-10-184-644-301
/ Sequence 301, Application US/10184644
/ Publication No. US20030044930A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C227
/ CURRENT APPLICATION NUMBER: US/10/184,644
/ CURRENT FILING DATE: 2002-06-28
/ Prior Application removed - See file wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 301
/ LENGTH: 1871
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-184-644-301

```

Query Match	27.6%	Score 60;	DB 14;	Length 1871;
Best Local Similarity	32.4%;	Pred. NO.	4.6e+02;	
Matches 12;	Conservative	3;	Mismatches 16;	Indels

Qy 1 ASCNGVCSPFEMPCCGTSACRCIPVGLVIGYCRNPSG 37
| : | : ||||| | | | |
Db 490 ATCAGCCT-----CGTCCCCCCCAGTAAAGCTGTAG 520

RESULT 14

```

US-10-184-634-301
; Sequence 301, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2003-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 301
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-301

```

Query Match 27.6%; Score 60; DB 14; Length 1871;
Best Local Similarity 32.4%; Pred.No. 4.6e+02;
Matches 12; Conservative 3; Mismatches 16; Indels

Qy 1 ASCNGVCSPFEMPCCGTSACRCIPVGLVIGYCRNPSG 37
| : | | : |||| | | | |
Db 490 ATCAGCCT-----CGTGTCCCCCAGTAAGCTGTAG 520

RESULT 15

```

US-10-063-685-91
; Sequence 91, Application US/10063685
; Publication No. US20030180909A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,685
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 91
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Homo Sapien

```


; APPLICANT: Stewart, Timothy A

```

; Publication No.. US20030148432A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/141,761
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-141-761-421

Query Match 27.4%; Score 59.5; DB 14; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

Qy 1 ASNGVCSPEMPPCGTSACRCIPVGLVIGYCRNPDSG 37
Db 440 AACTG-CGTGAGCGGTGACCCAGGCTTGCGTGAAG 475

RESULT 20
US-10-142-885-421
; Sequence 421, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA

```

```
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C153
; CURRENT APPLICATION NUMBER: US/10/137,871
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-871-421

Query Match      27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY      1 ASCNGVCSPPFMPPCGTSACRCIPVGLVIGYCRNPSG 37
      |||||
Db      440 AACTG-CGTGAGCGCGTGACCCAGGGCTTGCGTGAAG 475

RESULT 23
US-10-140-923-421
; Sequence 421, Application US/10140923
; Publication No. US2003020735A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C188
; CURRENT APPLICATION NUMBER: US/10/140,923
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-923-421

Query Match      27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY      1 ASCNGVCSPPFMPPCGTSACRCIPVGLVIGYCRNPSG 37
      |||||
Db      440 AACTG-CGTGAGCGCGTGACCCAGGGCTTGCGTGAAG 475

RESULT 24
US-10-141-756-421
; Sequence 421, Application US/10141756
; Publication No. US2003020735A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C197
; CURRENT APPLICATION NUMBER: US/10/141,759
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
```

```
; Sequence 421, Application US/10141756
; Publication No. US2003020735A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C200
; CURRENT APPLICATION NUMBER: US/10/141,756
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-756-421

Query Match      27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY      1 ASCNGVCSPPFMPPCGTSACRCIPVGLVIGYCRNPSG 37
      |||||
Db      440 AACTG-CGTGAGCGCGTGACCCAGGGCTTGCGTGAAG 475

RESULT 25
US-10-141-759-421
; Sequence 421, Application US/10141759
; Publication No. US20030207361A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C197
; CURRENT APPLICATION NUMBER: US/10/141,759
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:51:20 ; Search time 30 Seconds
(without alignments)
92.067 Million cell updates/sec

Title: US-09-674-496D-6

Perfect score: 217

Sequence: 1 ASNGVCSPEPMPGCTGTSACRCIPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	30.0	1073	4	US-09-949-016-9771
2	65	30.0	1104	2	US-08-327-832-5
3	65	30.0	1104	2	US-08-828-584-5
4	62	28.6	1798	4	US-09-845-583A-8
5	62	28.6	1798	4	US-09-561-709B-11
6	62	28.6	1798	4	US-09-917-254-87
7	61	28.1	291	4	US-09-902-540-15052
8	60.5	27.9	210	4	US-09-252-991A-20337
9	59	27.2	1799	4	US-09-845-583A-6
10	58.5	27.0	1101	4	US-09-561-709B-5
11	58.5	27.0	1761	4	US-09-561-709B-1
12	58	26.7	165	4	US-09-706-722A-10
13	57.5	26.5	581	4	US-09-244-805-27
14	56.5	26.0	998	4	US-09-252-991A-28424
15	56	25.8	41	3	US-08-836-686B-9
16	56	25.8	117	4	US-09-252-991A-17204
17	56	25.8	415	5	PCT-US93-00601-2
18	56	25.8	415	5	PCT-US94-07107A-2
19	56	25.8	425	5	PCT-US94-07107A-7
20	56	25.8	445	3	US-08-083-945C-2
21	55	25.3	445	3	US-08-083-945C-7
22	55	25.3	61	2	US-08-785-530-6
23	55	25.3	61	2	US-09-123-850-6
24	55	25.3	243	2	US-08-460-309-15
25	55	25.3	243	2	US-08-125-077-15
26	55	25.3	1854	4	US-09-949-016-11625
27	55	25.3	3075	2	US-08-460-309-5

28	55	25.3	3075	2	US-08-125-077-5	Sequence 5, Appli
29	54	24.9	64	4	US-09-270-767-59798	Sequence 59798, A
30	54	24.9	71	4	US-09-252-991A-20055	Sequence 20055, A
31	54	24.9	156	4	US-09-252-991A-22898	Sequence 22898, A
32	54	24.9	184	4	US-09-252-991A-25661	Sequence 25661, A
33	54	24.9	200	4	US-09-270-767-44372	Sequence 44372, A
34	53.5	24.7	2594	3	US-08-718-388-7	Sequence 7, Appli
35	53.5	24.7	5405	3	US-08-718-388-9	Sequence 9, Appli
36	53	24.4	37	3	US-08-836-686B-7	Sequence 7, Appli
37	53	24.4	75	4	US-09-489-039A-11668	Sequence 11668, A
38	53	24.4	254	4	US-09-586-106D-67	Sequence 67, Appli
39	53	24.4	3571	4	US-09-911-842A-2	Sequence 2, Appli
40	52.5	24.2	413	4	US-09-252-991A-23751	Sequence 23751, A
41	52.5	24.2	1754	1	US-07-745-206A-13	Sequence 13, Appli
42	52.5	24.2	1754	2	US-08-311-363-13	Sequence 13, Appli
43	52	24.0	41	3	US-08-836-686B-8	Sequence 8, Appli
44	52	24.0	400	2	US-08-103-170-9	Sequence 9, Appli
45	52	24.0	402	1	US-08-444-734A-6	Sequence 6, Appli
46	52	24.0	402	1	US-08-087-772A-15	Sequence 15, Appli
47	52	24.0	408	1	US-07-916-901-2	Sequence 2, Appli
48	52	24.0	408	1	US-08-351-473B-3	Sequence 3, Appli
49	52	24.0	408	3	US-08-450-962-2	Sequence 2, Appli
50	52	24.0	408	3	US-08-450-962-5	Sequence 5, Appli
51	52	24.0	408	4	US-08-848-631-2	Sequence 5, Appli
52	52	24.0	408	4	US-08-848-631-5	Sequence 5, Appli
53	52	24.0	1497	4	US-09-060-854B-2	Sequence 2, Appli
54	52	24.0	1497	4	US-09-529-904-3	Sequence 3, Appli
55	51.5	23.7	593	4	US-09-561-709B-13	Sequence 13, Appli
56	51.5	23.7	1342	4	US-09-561-709B-16	Sequence 16, Appli
57	51.5	23.7	1765	4	US-09-562-702A-16	Sequence 16, Appli
58	51.5	23.7	1786	4	US-09-562-702A-14	Sequence 14, Appli
59	51.5	23.7	1786	4	US-09-561-818A-14	Sequence 14, Appli
60	51.5	23.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
61	51.5	23.7	1786	4	US-09-538-092-869	Sequence 869, App
62	51.5	23.7	1786	4	US-08-469-486-52	Sequence 52, Appli
63	51.5	23.7	4544	2	US-08-469-486-52	Sequence 52, Appli
64	51.5	23.7	4544	2	US-09-489-039A-12891	Sequence 12891, A
65	51	23.5	243	2	US-08-460-309-16	Sequence 16, Appli
66	51	23.5	243	2	US-08-125-077-16	Sequence 16, Appli
67	51	23.5	281	4	US-09-248-796A-15282	Sequence 15282, A
68	51	23.5	344	1	US-08-689-974-1	Sequence 1, Appli
69	51	23.5	344	3	US-09-058-376-1	Sequence 1, Appli
70	51	23.5	690	4	US-09-371-338-19	Sequence 19, Appli
71	51	23.5	1652	4	US-09-627-650B-1	Sequence 1, Appli
72	51	23.5	1652	4	US-09-436-063C-1	Sequence 1, Appli
73	51	23.5	1652	4	US-09-627-650B-5	Sequence 5, Appli
74	51	23.5	1917	4	US-09-436-063C-5	Sequence 5, Appli
75	51	23.5	1917	4	US-09-627-650B-7	Sequence 7, Appli
76	51	23.5	2508	4	US-09-436-063C-7	Sequence 7, Appli
77	51	23.5	2508	4	US-09-627-650B-3	Sequence 3, Appli
78	51	23.5	2544	4	US-09-436-063C-3	Sequence 3, Appli
79	51	23.5	2544	4	US-09-627-650B-9	Sequence 9, Appli
80	51	23.5	2601	4	US-09-436-063C-9	Sequence 9, Appli
81	51	23.5	2601	4	US-09-252-991A-23483	Sequence 23483, A
82	50.5	23.3	181	4	US-09-252-991A-23169	Sequence 23169, A
83	50.5	23.3	306	4	US-09-907-794A-4	Sequence 4, Appli
84	50.5	23.3	379	4	US-09-905-125A-4	Sequence 4, Appli
85	50.5	23.3	379	4	US-09-902-775A-4	Sequence 4, Appli
86	50.5	23.3	379	4	US-09-906-700-4	Sequence 4, Appli
87	50.5	23.3	379	4	US-09-903-603A-4	Sequence 4, Appli
88	50.5	23.3	379	4	US-09-904-920A-4	Sequence 4, Appli
89	50.5	23.3	379	4	US-09-909-064-4	Sequence 4, Appli
90	50.5	23.3	379	4	US-09-905-381A-4	Sequence 4, Appli
91	50.5	23.3	379	4	US-09-906-618-4	Sequence 4, Appli
92	50.5	23.3	380	4	US-09-205-258-441	Sequence 441, App
93	50.5	23.3	380	4	US-08-836-686B-6	Sequence 6, Appli
94	50	23.0	50	3	US-08-836-686B-6	Sequence 6, Appli
95	50	23.0	51	3	US-08-836-686B-2	Sequence 2, Appli
96	50	23.0	61	2	US-08-785-530-1	Sequence 1, Appli
97	50	23.0	61	2	US-09-123-850-1	Sequence 1, Appli
98	50	23.0	61	2	US-09-949-016-6675	Sequence 6675, Ap
99	50	23.0	108	4	US-09-270-767-46529	Sequence 46529, A
100	50	23.0	108	4		

RESULT 2
US-08-327-832-5
; Sequence 5, Application US/08327832
; Patent No. 5840832
; GENERAL INFORMATION:
; APPLICANT: Ono, Santa J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: Transcription Factor Regulating MHC
; TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
; TITLE OF INVENTION: Retroviral Expression Contracts Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,832
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.46362
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 20-2 508-9153
; TELEFAX: 202 508-9299

US-09-845-583A-8
; Sequence 8, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:


```
Best Local Similarity 57.7%; Pred. No. 13;
Matches 15; Conservative 1; Mismatches 7; Indels 3; Gaps 2;

QY 1 ASCNGVCSPPFMPGCGTSACRCIPVG 26
Db 106 ASCSTTCS--TPPPCG-SACRDWPSG 128

RESULT 9
US-09-845-583A-6
; Sequence 6, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845.583A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-6

Query Match 27.2%; Score 59; DB 4; Length 1799;
Best Local Similarity 35.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 6 VCSPP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37
Db 816 VCATGYGFGPGACQACQCSPDGALSALCBGTSG 849

RESULT 10
US-09-561-709B-5
; Sequence 5, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-5

Query Match 27.0%; Score 58.5; DB 4; Length 1101;
Best Local Similarity 41.9%; Pred. No. 1e+02;
Matches 18; Conservative 2; Mismatches 10; Indels 13; Gaps 4;

QY 2 SC--NGVCSPPFMPGCG-----TSACRCIP--VGLVIGYC 32
Db 1023 SCHASGV-SPMECPGCGGACLCDPVTGACPCLEPNTGLACDRC 1064

RESULT 11
US-09-561-709B-1
; Sequence 1, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-1

Query Match 27.0%; Score 58.5; DB 4; Length 1761;
Best Local Similarity 41.9%; Pred. No. 1.6e+02;
Matches 18; Conservative 2; Mismatches 10; Indels 13; Gaps 4;

QY 2 SC--NGVCSPPFMPGCG-----TSACRCIP--VGLVIGYC 32
Db 1023 SCHASGV-SPMECPGCGGACLCDPVTGACPCLEPNTGLACDRC 1064

RESULT 12
US-09-706-722A-10
; Sequence 10, Application US/09706722A
; Patent No. 6670328
; GENERAL INFORMATION:
; APPLICANT: LASSALLE, PHILIPPE
; APPLICANT: MARCHANDISE, GENEVIEVE
; APPLICANT: KEROVAZE, GWENOLA
; APPLICANT: TONNEL, ANDRE BERNARD
; APPLICANT: MOLLET, SOPHIE
; TITLE OF INVENTION: PROTEINS AND PETIDES DERIVED FROM PROTEIN ESM-1 AND
; TITLE OF INVENTION: THEIR USES IN THE TREATMENT AND DIAGNOSIS OF DISEASES
; FILE REFERENCE: 8425/P-61263US2
; CURRENT APPLICATION NUMBER: US/09/706,722A
; CURRENT FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/102,909
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/050,614
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Laminin B2 (lmb2)
; OTHER INFORMATION: amino acid sequence
US-09-706-722A-10

Query Match 26.7%; Score 58; DB 4; Length 165;
Best Local Similarity 41.7%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 14 PGCTSACRCIPVGLVIGYCRNPSG 37
```

RESULT 17
PCT-US93-00601-2

; Sequence 2, Application PC/TUS9300601
; GENERAL INFORMATION:
; APPLICANT: Beckner, Marie E.
; APPLICANT: Liotta, Lance A.
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00601
; FILING DATE: 19930129
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-00601-2

Query Match 25.8%; Score 56; DB 5; Length 415;
Best Local Similarity 40.0%; Pred. No. 77;
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 4 NGVCSPPFEMPCCGTSACRCIPVG--LVIGY 31
DB 205 NGDCKTFQGNCPATCGRVLPDGKRAVVGY 234

RESULT 18
PCT-US94-07107A-2
; Sequence 2, Application PC/TUS9407107A
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of
; APPLICANT: America, as represented by the Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07107A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,043
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684

; REFERENCE/DOCKET NUMBER: 15280-156-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07107A-2

Query Match 25.8%; Score 56; DB 5; Length 415;
Best Local Similarity 40.0%; Pred. No. 77;
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 4 NGVCSPPFEMPCCGTSACRCIPVG--LVIGY 31
DB 205 NGDCKTFQGNCPATCGRVLPDGKRAVVGY 234

RESULT 19
PCT-US94-07107A-7
; Sequence 7, Application PC/TUS9407107A
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of
; APPLICANT: America, as represented by the Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07107A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,043
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-156-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07107A-7

Query Match 25.8%; Score 56; DB 5; Length 426;
Best Local Similarity 40.0%; Pred. No. 79;
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 4 NGVCSPPFEMPCCGTSACRCIPVG--LVIGY 31
DB 216 NGDCKTFQGNCPATCGRVLPDGKRAVVGY 245

RESULT 20
US-08-083-945C-2
; Sequence 2, Application US/08083945C
; Patent No. 6274134
; GENERAL INFORMATION:
; APPLICANT: Beckner, Marie E.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kruttsch, Henry C.
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,945C
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,043
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-156-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-083-945C-2

Query Match 25.8%; Score 56; DB 3; Length 445;
Best Local Similarity 40.0%; Pred. No. 82;
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
Qy 4 NGVSPFEMPCCGTSACRCIPVG--LVIGY 31
Db 216 NGDCKTFQGNPCATCGRVLDPGRVAVGY 245

RESULT 21
US-08-083-945C-7
; Sequence 7, Application US/08083945C
; Patent No. 6274134
; GENERAL INFORMATION:
; APPLICANT: Beckner, Marie E.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kruttsch, Henry C.
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,945C
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,043
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-156-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-083-945C-7

Query Match 25.8%; Score 56; DB 3; Length 445;
Best Local Similarity 40.0%; Pred. No. 82;
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
Qy 4 NGVSPFEMPCCGTSACRCIPVG--LVIGY 31
Db 216 NGDCKTFQGNPCATCGRVLDPGRVAVGY 245

RESULT 22
US-08-785-530-6
; Sequence 6, Application US/08785530
; Patent No. 5814480
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,530
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0194 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 305363
US-08-785-530-6

Query Match 25.3%; Score 55; DB 2; Length 61;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 12; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 2 SCNGVCSPPF--MPPCGTSAACRCPVPG 26
Db 14 SCGSGCKCKCKCTTCKKSCCSCCPVG 40

RESULT 23
US-09-123-850-6
; Sequence 6, Application US/09123850
; Patent No. 5955428
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,850
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0194 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 305363
US-09-123-850-6

Query Match 25.3%; Score 55; DB 2; Length 61;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 12; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 2 SCNGVCSPPF--MPPCGTSAACRCPVPG 26
Db 14 SCGSGCKCKCKCTTCKKSCCSCCPVG 40

RESULT 24
US-08-460-309-15
; Sequence 15, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-15

Query Match 25.3%; Score 55; DB 2; Length 243;
Best Local Similarity 44.0%; Pred. No. 60;
Matches 11; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 8 SPFMPGCTSAACRCPVGLVIGYC 32
Db 118 SPYEDEPC--RPCNCDPVGSLSSVC 140

RESULT 25
US-08-125-077-15
; Sequence 15, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-15

Query Match 25.3%; Score 55; DB 2; Length 243;
Best Local Similarity 44.0%; Pred. No. 60;
Matches 11; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 8 SPFEMPCGTACRCIPVGLVIGVC 32
Db 118 SPYDEPC--RPCNCDPVGSLSSVC 140

Search completed: March 28, 2005, 09:02:15
Job time : 31 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:39:59 ; Search time 92 Seconds
(without alignments)
155.545 Million cell updates/sec

Title: US-09-674-496d-6

Perfect score: 217

Sequence: 1 ASCNGVCSPEMPGCTGACRCIPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqpl1980s:*

2: Geneseqpl1990s:*

3: Geneseqpl2000s:*

4: Geneseqpl2001s:*

5: Geneseqpl2002s:*

6: Geneseqpl2003s:*

7: Geneseqpl2003bs:*

8: Geneseqpl2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	100.0	37	3	AY55990 Insectici
2	216	99.5	37	3	AY55991 Insectici
3	154	71.0	37	3	AY55992 Insectici
4	88	40.6	18	4	AAB85936 PA1b seed
5	88	40.6	18	8	ADO21580 Pea album
6	75	34.6	18	4	AAB85941 PA1b seed
7	75	34.6	18	8	AAB85941 PA1b seed
8	65	30.0	1024	5	ABO21585 Pea album
9	62	28.6	1024	5	ABO21585 Pea album
10	65	30.0	1104	2	AAR94957 NF-X1 DNA
11	63	29.0	838	4	ABB64668 Drosophil
12	62	28.8	564	8	ADP29241 Human sec
13	62	28.6	582	4	AM51816 Murine ap
14	62	28.6	1798	5	AAU84346 Protein L
15	62	28.6	1798	5	AAU84346 Protein L
16	61	28.1	94	3	AAG08039 Arabidops
17	61	28.1	94	3	AAG08039 Arabidops
18	61	28.1	96	3	AAG08038 Arabidops
19	61	28.1	96	3	AAG08037 Arabidops
20	61	28.1	114	3	AAG08037 Arabidops
21	61	28.1	114	3	AAG08037 Arabidops
22	60.5	27.9	210	7	ABO71791 Pseudomon
23	60.5	27.9	681	8	ADP30850 Human sec
24	60.5	27.9	915	8	ADP30957 Human sec
25	59.5	27.4	576	8	ADP29284 Human sec

26	59	27.2	1799	5	AAU50359	Aam50359	Mouse lam
27	59	27.2	1799	8	ADSI7495	Adsi7495	Amino aci
28	59	27.2	1799	8	ADR97664	Adr97664	Murine la
29	58.5	27.0	885	7	ADE08939	Ade08939	Novel pro
30	58.5	27.0	1029	8	ADN04730	Adn04730	Antipeori
31	58.5	27.0	1101	7	ADE28641	Ade28641	Human NOV
32	58.5	27.0	1101	8	ADM93386	Adm93386	Human NOV
33	58.5	27.0	1105	2	AAI15459	Aai15459	SEQ ID 5
34	58.5	27.0	1670	7	ADE07851	Ade07851	Novel pro
35	58.5	27.0	1761	2	AAI15457	Aai15457	Human lam
36	58	26.7	165	8	ADM24888	Adm24888	Laminin b
37	58	26.7	413	7	ABM85368	Abm85368	Mouse pro
38	58	26.7	1801	2	AAW50895	Aaw50895	Rat lamin
39	58	26.7	1801	7	ADE60383	Ade60383	Rat Prote
40	57.5	26.5	581	2	AAI42774	Aai42774	Rat neuro
41	57.5	26.5	581	4	AAW51819	Aaw51819	Rat apopt
42	57.5	26.5	7285	6	ABJ38280	Abj38280	PAMG21-RA
43	57	26.3	152	2	AAR12094	Aar12094	Antigenic
44	57	26.3	174	2	AAR12095	Aar12095	Antigenic
45	57	26.3	1579	4	ABBS8902	Abbs8902	Drosophil
46	57	26.3	4360	8	ADP30525	Adp30525	Human sec
47	56.5	26.0	152	2	AAR24045	Aar24045	Apolipop
48	56.5	26.0	271	7	ADJ92151	Adj92151	Human hai
49	56.5	26.0	998	7	ABO79678	AbO79678	Pseudomon
50	56	25.8	56	4	ABB65666	Abb65666	Drosophil
51	56	25.8	117	7	ABO88458	AbO88458	Pseudomon
52	56	25.8	141	4	AAU16536	Aau16536	Human nov
53	56	25.8	141	6	ABU55605	Abu55605	Human nov
54	56	25.8	377	4	ABB68017	Abb68017	Drosophil
55	56	25.8	415	2	AAR32922	Aar32922	AAMP-1
56	56	25.8	415	2	AAR66773	Aar66773	N-termina
57	56	25.8	426	2	AAR66776	Aar66776	Cell adhe
58	56	25.8	452	8	ABM80393	Abm80393	Tumour-as
59	56	25.8	452	8	ADR73434	Adr73434	Human ang
60	56	25.8	611	5	AAU82968	Aau82968	Human hom
61	55.5	25.6	92	5	ABG99510	Abg99510	Conus sp
62	55.5	25.6	137	4	AAU45020	Aau45020	Propionib
63	55.5	25.6	137	6	ABM41539	Abm41539	Propionib
64	55.5	25.6	238	7	ABM74267	Abm74267	DNA clone
65	55.5	25.6	318	4	AAG71666	Aag71666	Human olf
66	55.5	25.6	318	4	AAG72405	Aag72405	Human OR-
67	55.5	25.6	976	8	ADP30688	Adp30688	Human sec
68	55.5	25.6	1676	8	ADP30515	Adp30515	Human sec
69	55	25.3	42	4	ADG27736	Adg27736	Human nov
70	55	25.3	76	4	AAU66727	Aau66727	Propionib
71	55	25.3	76	4	AAU52006	Aau52006	Propionib
72	55	25.3	76	6	ABM48525	Abm48525	Propionib
73	55	25.3	76	6	ABM63246	Abm63246	Propionib
74	55	25.3	142	4	AAU33434	Aau33434	Propionib
75	55	25.3	142	6	ABM49953	Abm49953	Propionib
76	55	25.3	162	4	AAU14874	Aau14874	Peptide #
77	55	25.3	162	4	ABB33842	Abb33842	Peptide #
78	55	25.3	162	4	AAU27301	Aau27301	Peptide #
79	55	25.3	162	4	ABB28658	Abb28658	Peptide #
80	55	25.3	162	4	ABBI9284	Abbi9284	Protein #
81	55	25.3	162	4	ABM67014	Abm67014	Human bon
82	55	25.3	162	4	AAU54608	Aau54608	Human bra
83	55	25.3	162	4	ABG48677	Abg48677	Human liv
84	55	25.3	162	4	AAU02599	Aau02599	Peptide #
85	55	25.3	162	5	ABG36671	Abg36671	Human pep
86	55	25.3	171	6	ABU70429	Abu70429	Human adi
87	55	25.3	642	4	AAU00786	Aau00786	Human bon
88	55	25.3	1216	4	ABG09754	Abg09754	Novel hum
89	55	25.3	1543	5	ADI16784	Adi16784	Human NOV
90	55	25.3	1543	8	ADN42438	Adn42438	Human nov
91	55	25.3	1555	7	ADC39156	Adc39156	Novel hum
92	55	25.3	1585	8	ADH72284	Adh72284	Human pro
93	55	25.3	1566	7	ADC39166	Adc39166	Novel hum
94	55	25.3	1566	8	ADH72294	Adh72294	Human pro
95	55	25.3	1789	8	ADP31028	Adp31028	Human sec
96	55	25.3	1798	7	AAW50896	Aaw50896	Human lam
97	55	25.3	1798	7	ADE60385	Ade60385	Human pro
98	55	25.3	2901	4	ABG09763	Abg09763	Novel hum

99	55	25.3	3075	2	AAW50892	Human lam
100	54.5	25.1	63	8	ADI34568	Human ins

ALIGNMENTS

RESULT 1
AAY55990
ID AAY55990 standard; peptide; 37 AA.

AC AAY55990;

DT 15-MAR-2000 (first entry)

DE Insecticidal peptide PT from pea plants.

Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;
pest; *Sitophilus oryzae*; *Ephestia kuehniella*; *Acyrtosiphon pisum*;
genetically modified organism.

OS Pisum sativum.

XX
PN
W09958695-A1.

18-NOV-1999

07-MAY-1999: 99WO-FR001085

XX
PR 11-MAY-1998: 98ER-00005877

XX (NASC-) INST NAT SCI APPLIQUEES LYON.
PA (INRG) INST NAT RECH AGRONOMIQUE.

PI Delobel B, Grenier A, Guequen J, Ferrasson E, Mbaïlao M:

DR WPI; 2000-062304/05.

Use of polypeptide as insecticide, especially for controlling cereal grain pests.

PS Example 2; Fig 7; 38pp; French.

This sequence represents the Cys-rich peptide sequence of legume plant derived insecticidal peptide PT corresponding to that of an entomotoxic pea protein. The peptide has homology to the known insecticidal peptides PALB (AAV55991) from peas or leguminsine (AAV55992) from soybeans. The insecticidal peptides preferably have the amino acid sequence:

CC amino acids; X1 = 2-10 amino acids; X2 = 2-5
CC amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
CC acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
CC peptide can be used to protect cereal products or plants from attack by
CC cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
CC Acyrthosiphon pisum, either directly or by genetically modifying plants
CC (especially cereal plants) to express the peptide in their tissues or
CC organs
XX
SQ Sequence 37 RA: SQ

RESULT 2
 AAY55991
 ID AAY55991 standard; peptide; 37 AA.
 XX
 AC AAY55991;

XX
DT 15-MAR-2000 (first entry)
XX
DE Insecticidal peptide P11b from pea plants.

KW Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;
KW pest; *Sitophilus oryzae*; *Ephestia kuehniella*; *Acyrtosiphon pisum*;
KW genetically modified organism.

OS Pisum sativum.

AA
PN
WO9958695-A1

18-NOV-1999

XX
PF 07-MAY-1999: 99WQ-FR001085XX
PR 11-MAY-1998. 98EP-00005877

XX
PA (NASC-) INST NAT SCI APPLIQUEES LYON.
PA (INRG) INST NAT RECH AGRONOMIQUE.

PI Delobel B, Grenier A, Guequen J, Ferrasson E, Mbailao M:

WPI; 2000-062304/05.

Use of polypeptide as insecticide, especially for controlling cereal grain pests.

XX Example 2; Fig 7; 38pp: French.
PS

This sequence represents the Cys-rich peptide sequence of legume plant
 derived insecticidal peptide Pa1b corresponding to that of an entomotoxic
 pea protein. The invention relates to a novel insecticidal peptide P1
 (AAV55990) isolated from pea plants which has homology to the Pa1b
 peptide and to the leguminsine from soybeans (AAV55991). The insecticidal
 peptides preferably have the amino acid sequence:

CC amino acids; X1 = 2-10 amino acids; X2 = 2-5
CC amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4
CC amino acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
peptide can be used to protect cereal products or plants from attack by
cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
Acarthosia pismum, either directly or by genetically modifying plants
(especially cereal plants) to express the peptide in their tissues or
organs

RESULT 3
AAY55992
ID AAY55992 standard; peptide: 37 AA.

AA
AC
AAAY55992;XX
DT 15-MAR-2000 (first entry)

XX Insecticidal peptide leginsuline form soybean plants. DE

KW Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;
KW pest; *Sitophilus oryzae*; *Ephesia kuehniella*; *Acyrtosiphon pisum*;
KW genetically modified organism.

Glycine max.

```

PN WO9958695-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-FR001085.
XX
XX 11-MAY-1998; 98FR-00005877.
XX
XX (NASC-) INST NAT SCI APPLIQUEES LYON.
XX (INRG) INST NAT RECH AGRONOMIQUE.
XX
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;
XX
XX WPI; 2000-062304/05.
XX
XX Use of polypeptide as insecticide, especially for controlling cereal
XX grain pests.
XX
XX Example 2; Fig 7; 38pp; French.
XX
XX This sequence represents the Cys-rich peptide sequence of legume plant
XX derived insecticidal peptide leginsuline corresponding to that of an
XX entomotoxic pea protein. The invention relates to a novel insecticidal
XX peptide PT (AAV55990) isolated from pea plants which has homology to the
XX P1b peptide (AAV55991) and to the leginsuline from soybeans. The
XX insecticidal peptides preferably have the amino acid sequence:
XX X1CYSX2CYEX3CYSX4CYSX5CYSX6CYEX7, where X1 = 2-10 amino acids; X2 = 2-5
XX amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
XX acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
XX peptides can be used to protect cereal products or plants from attack by
XX cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
XX Acyrthosiphon pisum, either directly or by genetically modifying plants
XX (especially cereal plants) to express the peptide in their tissues or
XX organs
XX
XX Sequence 37 AA;

Query Match 71.0%; Score 154; DB 3; Length 37;
Best Local Similarity 59.5%; Pred. No. 2.8e-09;
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ASCNGVCSPPFPCGTSACRCIPVGLVIGYCRNPSG 37
Db 1 ADCNGACSPFVPCRCRDCRCVPIGLVFGCIHPTG 37

RESULT 4
AAB85936
ID AAB85936 standard; peptide; 18 AA.
XX
XX AAB85936;
XX
XX 30-NOV-2001 (first entry)
XX
XX P1b seed storage protein fragment.
XX
XX Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
XX 2A11; P1A1b.
XX
XX Unidentified.
XX
XX USC281410-B1.
XX
XX 28-AUG-2001.
XX
XX 15-JAN-1999; 99US-00232861.
XX
XX 31-JUL-1986; 86US-00891529.
XX 26-MAY-1987; 87US-00054369.
XX 28-JUL-1987; 87US-00078538.
XX 25-JAN-1988; 88US-00147781.
XX 15-MAR-1988; 88US-00168190.
XX 29-APR-1988; 88US-00188361.

02-NOV-1988; 88US-00267685.
21-MAY-1990; 90US-00526123.
09-JUL-1990; 90US-00550804.
10-AUG-1993; 93US-00105852.
07-JUN-1995; 95US-00484941.
07-MAR-1997; 97US-00812665.
XX
XX (CALJ) CALGENE LLC.
XX
XX Knauf VC, Kridl JC;
XX
XX WPI; 2001-564354/63.
XX
XX Obtaining a plant that produces a seed with a modified phenotype or
XX altering a seed phenotype, comprises transforming a plant cell with a DNA
XX construct consisting of operably linked components in the direction of
XX transcription.
XX
XX Example 9; Fig 6; 68pp; English.
XX
XX The invention provides a method for obtaining a plant which produces at
XX least one seed having a modified phenotype. The method involves
XX transforming a host plant cell with a DNA construct which consists of
XX operably linked components in the direction of transcription, a promoter
XX region from a Brassica plant gene, a DNA sequence of interest other than
XX the native coding sequence, and a transcription termination region. The
XX method is useful for obtaining plants having modified phenotype or for
XX altering the phenotype of a plant seed or tissue. The DNA constructs are
XX used in manipulating plant cells to provide for regulated transcription,
XX such as light inducible transcription, in a plant tissue or plant part of
XX interest at particular stages of plant growth or in response to external
XX control. These constructs are also used for modulation of expression of
XX endogenous products as well as production of exogenous products in the
XX seed. Sequences AAB85936-39 represent fragments of storage proteins used
XX in comparison studies with the storage protein 2A11
XX
XX Sequence 18 AA;

Query Match 40.6%; Score 88; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.015;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VCSPPFPCGTSACRCI 23
Db 1 VCSPPFPCGTSACRCI 18

RESULT 5
ADO21580
ID ADO21580 standard; peptide; 18 AA.
XX
XX ADO21580;
XX
XX 01-JUL-2004 (first entry)
XX
XX Pea albumin 1b reactive site.
XX
XX Pea; fruit specific promoter; plant; transgenic; protein storage;
XX improved nutrient source; enhanced response to light;
XX dehydration resistance; herbicide resistance; pest resistance; 2A11 gene;
XX protease inhibitor.
XX
XX Pisum sativum.
XX
XX OS
XX
XX US2004055038-A1.
XX
XX 18-MAR-2004.
XX
XX 12-FEB-2001; 2001US-00782130.
XX
XX 17-JAN-1985; 85US-00692605.
XX 31-JUL-1986; 86US-00891529.
XX 26-MAY-1987; 87US-00054369.

```

PR 28-JUL-1987; 87US-00078538.
 PR 15-JAN-1988; 88US-00147781.
 PR 25-MAR-1988; 88US-00168190.
 PR 29-APR-1988; 88US-00188361.
 PR 02-NOV-1988; 88US-00267685.
 PR 21-MAY-1990; 90US-00526123.
 PR 09-JUL-1990; 90US-00550804.
 PR 14-SEP-1990; 90US-00582241.
 PR 08-AUG-1991; 91US-00742834.
 PR 10-AUG-1993; 93US-00105852.
 PR 07-JUN-1995; 95US-00484941.
 PR 07-MAR-1997; 97US-00812665.
 PR 15-JAN-1999; 99US-00232861.
 XX (KNAU/) KNAUF V C.
 PA (KRIDL/) KRIDL J C.
 XX Knauf VC, Kridl JC;
 XX WPI; 2004-247819/23.
 XX New DNA construct comprising a promoter region, a DNA sequence of
 PT interest and a transcription termination region, useful for producing
 PT transgenic plants.
 XX Example 9; Fig 6; 68pp; English.
 XX The invention relates to a DNA construct comprising, as operably linked
 CC components in the direction of transcription, a promoter region
 CC obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier
 CC protein (ACP) gene, a DNA sequence of interest other than the native
 CC coding sequence of the gene and a transcription termination region, where
 CC the components are functional in a plant cell and where the DNA construct
 CC is flanked by T-DNA. Also included are a plant cell having an altered
 CC phenotype as a result of expression of a DNA construct, a plant
 CC comprising cells comprising a DNA construct, a seed obtained from the
 CC plant, obtaining a plant having a modified phenotype or modifying the
 CC genotype of a plant to impart a desired characteristic to seed as
 CC distinct from other plant tissue, altering the phenotype of plant seed
 CC tissue or modifying transcription in seed tissue as distinct from other
 CC plant tissue and selectively expressing a heterologous DNA sequence of
 CC interest in seed tissue as distinct from other plant tissue. The DNA
 CC construct is useful in modifying or altering the genotype or phenotype of
 CC a plant to impart a desired characteristic. The construct is also useful
 CC in regulating specific modification of plant or regulating tissue and/or
 CC developmental specific transcription and expression in plants. The plants
 CC produced have increased capability of protein storage, improved nutrient
 CC source, enhanced response to light and dehydration resistance and
 CC resistant to herbicide and pests. The seed specific promoters are from
 CC the Napin, ACP and EA9 genes and the fruit specific promoter is from the
 CC tomato 2A11 gene. The present sequence is a reactive site from a protein
 CC similar to the tomato 2A11 protein (thought to be a protease inhibitor).
 XX Sequence 18 AA;
 SQ Query Match 40.6%; Score 88; DB 8; Length 18;
 Best Local Similarity 72.2%; Pred. No. 0.015;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 VCSPFEMPCCGTSACRCI 23
 DB 1 VCSPFDIPPCGSLCRCI 18
 RESULT 6
 AAB85941
 ID AAB85941 standard; peptide; 18 AA.
 XX AAB85941;
 XX 30-NOV-2001 (first entry)
 DT PA1b seed storage protein fragment.
 XX

XX Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
 KW 2A11; PALB.
 XX Unidentified.
 OS US6281410-B1.
 PN 28-AUG-2001.
 PD 15-JAN-1999; 99US-00232861.
 PF 31-JUL-1986; 86US-00891529.
 XX 26-MAY-1987; 87US-00054369.
 PR 28-JUL-1987; 87US-00078538.
 PR 25-JAN-1988; 88US-00147781.
 PR 15-MAR-1988; 88US-00168190.
 PR 29-APR-1988; 88US-00188361.
 PR 02-NOV-1988; 88US-00267685.
 PR 21-MAY-1990; 90US-00526123.
 PR 09-JUL-1990; 90US-00550804.
 PR 10-AUG-1993; 93US-00105852.
 PR 07-JUN-1995; 95US-00484941.
 PR 07-MAR-1997; 97US-00812665.
 XX (CALJ) CALGENE LLC.
 XX Knauf VC, Kridl JC;
 PI WPI; 2001-564354/53.
 DR Obtaining a plant that produces a seed with a modified phenotype or
 XX altering a seed phenotype, comprises transforming a plant cell with a DNA
 PT construct consisting of operably linked components in the direction of
 PT transcription.
 XX Example 9; Fig 6; 68pp; English.
 XX The invention provides a method for obtaining a plant which produces at
 CC least one seed having a modified phenotype. The method involves
 CC transforming a host plant cell with a DNA construct which consists of
 CC operably linked components in the direction of transcription, a promoter
 CC region from a Brassica plant gene, a DNA sequence of interest other than
 CC the native coding sequence, and a transcription termination region. The
 CC method is useful for obtaining plants having modified phenotype or for
 CC altering the phenotype of a plant seed or tissue. The DNA constructs are
 CC used in manipulating plant cells to provide for regulated transcription,
 CC such as light inducible transcription, in a plant tissue or plant part of
 CC interest at particular stages of plant growth or in response to external
 CC control. These constructs are also used for modulation of expression of
 CC endogenous products as well as production of exogenous products in the
 CC seed. Sequences AAB85941-47 represent fragments of storage proteins used
 CC in comparison studies with the storage protein 2A11
 XX Sequence 18 AA;
 SQ Query Match 34.6%; Score 75; DB 4; Length 18;
 Best Local Similarity 72.2%; Pred. No. 0.35;
 Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 16 GTSACRCIPVGLVIGYCR 33
 DB 1 GSPLCRCIPAGLVIGNCR 18
 RESULT 7
 ADO21585
 ID ADO21585 standard; peptide; 18 AA.
 XX ADO21585;
 XX 01-JUL-2004 (first entry)
 DT
 XX

DE Pea albumin 1b N-terminus.

XX Pea; fruit specific promoter; plant; transgenic; protein storage;

KW improved nutrient source; enhanced response to light;

KW dehydration resistance; herbicide resistance; pest resistance; 2A11 gene;

XX protease inhibitor.

XX Pisum sativum.

OS

XX US2004055038-A1.

XX 18-MAR-2004.

XX

XX 12-FEB-2001; 2001US-00782130.

XX

XX 17-JAN-1985; 85US-00692605.

PR 31-JUL-1986; 86US-00891529.

PR 26-MAY-1987; 87US-00054369.

PR 28-JUL-1987; 87US-00078538.

PR 25-JAN-1988; 88US-00477781.

PR 15-MAR-1988; 88US-00168190.

PR 29-APR-1988; 88US-00188361.

PR 02-NOV-1988; 88US-00267685.

PR 21-MAY-1990; 90US-00526123.

PR 09-JUL-1990; 90US-00550804.

PR 14-SEP-1990; 90US-00582241.

PR 08-AUG-1991; 91US-00742834.

PR 10-AUG-1993; 93US-00105852.

PR 07-JUN-1995; 95US-00484941.

PR 07-MAR-1997; 97US-00812665.

PR 15-JAN-1999; 99US-00232861.

XX (KNAU//) KNAUF V C.

PA (KRIDL//) KRIDL J C.

XX

XX Knauf VC, Kridl JC;

XX

XX WPI; 2004-247819/23.

XX

XX New DNA construct comprising a promoter region, a DNA sequence of interest and a transcription termination region, useful for producing transgenic plants.

XX

XX Example 9; Fig 6; 68pp; English.

XX

XX The invention relates to a DNA construct comprising, as operably linked components in the direction of transcription, a promoter region obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier protein (ACP) gene, a DNA sequence of interest other than the native coding sequence of the gene and a transcription termination region, where the components are functional in a plant cell and where the DNA construct is flanked by T-DNA. Also included are a plant cell having an altered phenotype as a result of expression of a DNA construct, a plant comprising cells comprising a DNA construct, a seed obtained from the plant, obtaining a plant having a modified phenotype or modifying the genotype of a plant to impart a desired characteristic to seed as distinct from other plant tissue, altering the phenotype of plant seed tissue or modifying transcription in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue. The DNA construct is useful in modifying or altering the genotype or phenotype of a plant to impart a desired characteristic. The construct is also useful in regulating genetic modification of plant or regulating tissue and/or developmental specific transcription and expression in plants. The plants produced have increased capability of protein storage, improved nutrient source, enhanced response to light and dehydration resistance and resistant to herbicide and pests. The seed specific promoters are from the Napin, ACP and EA9 genes and the fruit specific promoter is from the tomato 2A11 gene. The present sequence is the N-terminus from a protein similar to the tomato 2A11 protein (thought to be a protease inhibitor).

XX

XX Sequence 18 AA;

XX

Query Match 34.6%; Score 75; DB 8; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.35;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 16 GTSACRCIPVGLVIGYCR 33
: ||||| ||||| ||
Db 1 GSPLCRCIPAGLVIGNCR 18

RESULT 8
ABB05595
ID ABB05595 standard; protein; 1024 AA.
XX
AC ABB05595;
XX
DT 23-APR-2002 (first entry)
XX
DE Human nuclear transcription factor 2 (NFX2) protein.
XX
KW Human; nuclear transcription factor 2; NFX2; chromosome 9; gene therapy.
XX
OS Homo sapiens.
XX
PN CN1318556-A.
XX
PD 24-OCT-2001.
XX
PF 11-APR-2001; 2001CN-00113502.
XX
PR 11-APR-2001; 2001CN-00113502.
XX
PA (UYNA-) UNIV NANJING MEDICAL.
XX
PI Sha J, Zhou Z, Li J;
XX
XX WPI; 2002-115093/16.
DR N-PSDB; ABA93409.
XX
XX Human nuclear transcription factor-2 gene encoded protein, useful for treating related disease.
XX
XX Claim 1; Page 1 (Claims); 7pp; Chinese.
XX
XX The present sequence represents the human nuclear transcription factor-2, designated NFX2. The NFX2 gene has a cDNA sequence of 3613 base pairs (bp) containing an open reading frame sequence of 3075 bp from position 62 to 3136, encoding a sequence of 1024 amino acids and having a Genbank number of AF332009. The present invention also describes: (1) utilising the NFX2 gene to prepare a fusion protein; (2) utilising the protein to immunise an animal and to prepare monoclonal and polyclonal antibodies; and (3) utilising the gene in preparing testicular specific function gene expressing chips. The expressed protein may be useful in gene therapy for treating related disease. The NFX2 gene has been located to human chromosome 9

XX

XX Query Match 30.0%; Score 65; DB 5; Length 1024;
Best Local Similarity 34.1%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 15; Indels 10; Gaps 3;

Qy 2 SCNGVCSPFEMPPCG-----TSACRC-----IPVGLVIG-YCRNP 35
: ||||| ||||| : : : : :
Db 456 SCNLLCHPGPCPCPFMTKTCGRTTRHTVRCQAVSVHCNSP 499

RESULT 9
ADJ69675
ID ADJ69675 standard; protein; 1024 AA.
XX
AC ADJ69675;
XX
DT 06-MAY-2004 (first entry)

Matches	12;	Conservative	4;	Mismatches	15;	Indels	2;	Gaps	1;
QY	7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37								
	:	:	:	:	:	:	:	:	
DB	816 CAPGYGFGPTGCGACQCSPRGALLCERTSG 848								
	:	:	:	:	:	:	:	:	
RESULT 15									
AAAM50360	ID								
XX	AAAM50360 standard; protein; 1798 AA.								
XX	AC								
XX	AAAM50360;								
AC	18-FEB-2002 (first entry)								
DT	Human laminin-15 beta 2 chain.								
XX									
XX	Laminin-15; human; retina; eye; therapy; ophthalmological;								
KW	antiinflammatory; rod dystrophy; rod-cone dysrophy;								
KW	retinitis pigmentosa; macular degeneration; retinal detachment.								
KW									
XX	OS								
XX	Homo sapiens.								
PN	WQ200183516-A1.								
XX									
XX	08-NOV-2001.								
PD									
XX	01-MAY-2001; 2001WO-US013943.								
PF									
XX									
XX	01-MAY-2000; 2000US-0200863P.								
PR									
XX									
XX	(MASS-) MASSACHUSETTS GEN HOSPITAL.								
PA									
XX									
XX	Burgeson RE, Brunken W, Champliaud M, Hunter D;								
PI									
XX									
DR	WPI; 2002-041478/05.								
DR	N-PSDB; AAI70819.								
XX									
XX	Novel substantially pure preparation comprising laminin having laminin chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders such as retinitis pigmentosa, macular degeneration, retinal detachment.								
PT									
PT									
PT									
XX	Disclosure; Fig 4A; 58pp; English.								
PS									
XX									
CC	The present sequence is that of the beta 2 chain of human laminin-15, a novel member of the laminin family that is produced in the retina. The retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2, gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed within the inter-photoreceptor matrix and in the outer plexiform layer, and may serve to stabilise retinal synapses. The invention provides laminin-15 preparations and cells comprising a nucleic acid encoding the laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of producing laminin-15. The laminin-15 preparation is used in claimed methods of: increasing retina immunophotoreceptor matrix stability; increasing the stability of retina photoreceptor compounds, especially an outer segment, inner segment or synapse; increasing retina adhesion; treating a disorder associated with retina degeneration, especially rod dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration and retinal detachment; increasing the stability of synapses of the central nervous system or peripheral nervous system; stimulating neuroregeneration, axon outgrowth or synapse formation; preparing an implant, e.g. a catheter, artificial joint, retinal implant, timed releasing device, neural cell growth guide or artificial tissue, by coating with the laminin-15 preparation; and increasing photosensitivity by implanting a tip coated with the laminin-15 preparation into an eye. The laminin may be recombinant, and the 3 chains co-expressed in the same cell or expressed in different cells								
XX									
XX	Sequence 1798 AA;								
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									
XX									

PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 18-JUL-1999; 99US-0144325P.
PR 18-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.

PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 28.1%; Score 61; DB 3; Length 94;
Best Local Similarity 35.7%; Pred. NO. 45;
Matches 15; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

QY 7 CSPFEMPPCGT-----SACRCIV-----SACRCIV-----GLVIGYCRNPS 36

Db 29 CSPMQLSPCAITATSSPPSALCCCAKKEQRPCLCGYMRNPS 70

RESULT 17


```
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0158369P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157553P.
PR 06-OCT-1999; 99US-0157855P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
```

Query Match 28.1%; Score 61; DB 3; Length 94;

Best Local Similarity 35.7%; Pred. No. 45;

Matches 15; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

```
QY 7 CSPFMPCCGT-----SACRCIPV-----GLVIGCRNPS 36
   |||::|||
Db 29 CSPMQLSPCATITSSPPSPALCCAKLKEQRPCLCGYMRNPS 70
   |||::|||
```

RESULT 18

AAG08038
ID AAG08038 standard; protein; 96 AA.XX
AC AAG08038;XX
DT 17-OCT-2000 (first entry)

XX

```
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5420.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
PN 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 17-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
```

PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142803P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145119P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145226P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145931P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.

PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 29-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 28.1%; Score 61; DB 3; Length 96;
Best Local Similarity 35.7%; Pred. No. 46;
Matches 15; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

Qy 7 CSPFEMPCTGCT-----SACRCIPV-----GLVIGYCRNPS 36
|||::|||:|||||
Db 31 CSPQLSPCATATSSSPSALCAKLEQRPCLCGYMRNPS 72

RESULT 19

AAG37330
ID AAG37330 standard; protein; 96 AA.
XX
AC AAG37330;
XX
DT 18-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 45883.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.

PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135112P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135623P.
PR 27-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137232P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 26-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158212P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.

PR	02-MAY-2003; 2003US-0467199P.	
PR	02-MAY-2003; 2003US-0467201P.	
PR	02-MAY-2003; 2003US-0467203P.	
PR	19-MAY-2003; 2003US-0467230P.	
PR	19-MAY-2003; 2003US-0471306P.	
PR	19-MAY-2003; 2003US-0471336P.	
PR	22-MAY-2003; 2003US-0472420P.	
PR	22-MAY-2003; 2003US-0472430P.	
PR	09-JUN-2003; 2003US-0476609P.	
PR	09-JUN-2003; 2003US-0476641P.	
PR	08-JUL-2003; 2003US-0485218P.	
PR	08-JUL-2003; 2003US-0485224P.	
PR	08-JUL-2003; 2003US-0485223P.	
PR	08-JUL-2003; 2003US-0485224P.	
PR	08-JUL-2003; 2003US-0485225P.	
PR	14-JUL-2003; 2003US-0486446P.	
PR	14-JUL-2003; 2003US-0486448P.	
PR	15-JUL-2003; 2003US-0486480P.	
PR	15-JUL-2003; 2003US-0486481P.	
PR	15-JUL-2003; 2003US-0486482P.	
PR	15-JUL-2003; 2003US-0486483P.	
PR	08-AUG-2003; 2003US-0493337P.	
PR	08-AUG-2003; 2003US-0493357P.	
PR	08-AUG-2003; 2003US-0493373P.	
XX	(FIVE-) FIVE PRIME THERAPEUTICS INC.	
PA	Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;	
PI	Halenbeck RF, Huang WM, Kotahkota S, Haishan L, Linemann T;	
PI	Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;	
XX	WPI; 2004-348438/32.	
XX	New nucleic acid molecule for diagnosing, preventing or treating diseases	
PT	such as proliferative (e.g. cancer), inflammatory, immune, metabolic,	
PT	genetic, bacterial and viral diseases.	
XX	Claim 1; SEQ ID NO 2955; 428pp; English.	
PS	The present invention relates to an isolated nucleic acid molecule	
CC	encoding a polypeptide which is believed to be cytostatic,	
CC	antiinflammatory, immunosuppressive, antibacterial and virucidal. The	
CC	composition and methods are useful for diagnosing, preventing and	
CC	treating diseases such as proliferative (e.g. cancer), inflammatory,	
CC	immune, metabolic, genetic, bacterial and viral diseases. The present	
CC	sequence represents a human secreted protein. The present sequence is	
CC	available on WIPOWEB and is not in the specification.	
XX	Sequence 915 AA;	
SQ	Query Match 27.9%; Score 60.5; DB 8; Length 915;	
	Best Local Similarity 37.5%; Pred. No. 3.7e+02;	
	Matches 12; Conservative 2; Mismatches 15; Indels 3; Gaps 1;	
QY	1 ASCNGVCSPPMPPCGTSACRCIPVLGVGYC 32	
DB	270 ATCGCGCGTGGCTCGTTTCATG---GCC 298	
RESULT 25		
ADP29284	ID ADP29284 standard; protein; 576 AA.	
XX	ADP29284;	
XX	AC AC	
DT	12-AUG-2004 (first entry)	
XX	Human secreted protein SEQ ID #51.	
DE	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KW	cancer; inflammatory; immune; human secreted protein.	
XX	Homo sapiens.	
OS	WO2004035732-A2.	
PN		

XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Hallenbeck RF, Huang WM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
DR
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 1282; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC anti-inflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPWEB and is not in the specification.
XX
SQ Sequence 576 AA;
Query Match 27.4%; Score 59.5; DB 8; Length 576;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
QY 15 CGTSACR-CIPVGLVIGYCRNPSG 37
Db 108 CGIKSCRGFLDQGLDDNYCRNPDG 131
Search completed: March 28, 2005, 08:57:08
Job time : 97 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:40:49 ; Search time 84 Seconds
(without alignments)
225.559 Million cell updates/sec

Title: US-09-674-496d-8

Perfect score: 222

Sequence: 1 ADCNGACSPPEVPPCRSDRCVPIGLVFGFCHPTG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	222	100.0	119	1	ALB1_SOYBN	Q9837 glycine max
2	216	97.3	119	1	ALB1_GLYSO	Q92X0 glycine soj
3	208	93.7	100	2	Q7XZC3	Q7XZC3 glycine max
4	192	86.5	89	1	ALB1_PHAHU	Q9FRT8 phaseolus a
5	169	76.1	96	2	Q6A1C7	Q6A1C7 vicia hirsu
6	168	75.7	140	2	Q7XZC5	Q7XZC5 medicago tr
7	165	74.3	130	1	AL1B_PEA	P62927 pisum sativ
8	163	73.4	100	2	Q6A1D7	Q6A1D7 astragalus
9	161.5	72.7	90	1	ALB1_PHAAN	Q9FRT9 phaseolus a
10	161	72.5	91	2	Q6A1D6	Q6A1D6 alysicarpus
11	161	72.5	130	1	AL1D_PEA	P62929 pisum sativ
12	158	71.2	98	2	Q6A1C9	Q6A1C9 onobrychis
13	158	71.2	130	1	AL1E_PEA	P62930 pisum sativ
14	155	69.8	130	1	AL1A_PEA	P62926 pisum sativ
15	154	69.4	99	2	Q6A1C8	Q6A1C8 trigonella
16	154	69.4	130	1	AL1F_PEA	P62931 pisum sativ
17	152	68.5	98	2	Q6A1D4	Q6A1D4 canavalia b
18	151	68.0	99	2	Q6A1D5	Q6A1D5 bituminaria
19	148.5	66.9	109	2	Q7XZC2	Q7XZC2 phaseolus v
20	137.5	61.9	101	2	Q6A1D3	Q6A1D3 lonchocarpu
21	136	61.3	130	1	AL1C_PEA	P62928 pisum sativ
22	128	57.7	98	2	Q6A1D2	Q6A1D2 melilotus a
23	125	56.3	81	1	ALB1_LUPAN	Q96474 lupinus ang
24	124.5	56.1	101	2	Q6A1D1	Q6A1D1 mundulea se
25	121	54.5	142	2	Q7XZC4	Q7XZC4 medicago tr
26	109	49.1	58	2	Q6A1B9	Q6A1B9 vigna ungui
27	109	49.1	58	2	Q6A1C0	Q6A1C0 vigna subte
28	103	46.4	59	2	Q6A1C3	Q6A1C3 lathyrus la
29	99.5	44.8	101	2	Q6A1D0	Q6A1D0 mundulea se
30	88	39.6	60	2	Q6A1C2	Q6A1C2 mundulea se
31	83	37.4	58	2	Q6A1C4	Q6A1C4 canavalia b

32	83	37.4	59	2	Q6A1C6	Q6A1C6 bituminaria
33	80	36.0	60	2	Q6A1C1	Q6A1C1 onobrychis
34	72	32.4	58	2	Q6A1C5	Q6A1C5 caragana ar
35	69	31.1	370	2	Q7Q894	Q7Q894 giardia lam
36	64	28.8	536	2	Q8IHD9	Q8IHD9 drosophila
37	64	28.8	539	2	Q8MLS4	Q8MLS4 drosophila
38	63	28.4	3075	1	LMAL_HUMAN	LMAL_HUMAN
39	62.5	28.2	379	1	WIFI_HUMAN	WIFI_HUMAN
40	62.5	28.2	379	2	Q6UX11	Q6UX11 homo sapien
41	61.5	27.7	1847	2	Q76952	Q76952 aedes aegyp
42	60.5	27.3	220	2	Q99KR2	Q99KR2 mus musculu
43	60.5	27.3	365	2	Q924V6	Q924V6 rattus norv
44	60.5	27.3	379	1	WIFI_MOUSE	WIFI_MOUSE
45	60.5	27.3	379	2	Q6IM38	Q6IM38 mus musculu
46	59	26.6	3084	1	LMAL_MOUSE	LMAL_MOUSE
47	58.5	26.4	592	2	Q7QT99	Q7QT99 giardia lam
48	58	26.1	494	2	Q6DU29	Q6DU29 xenopus tro
49	57.5	25.9	87	1	OM3_CHLPS	OM3_CHLPS
50	57.5	25.9	421	2	Q7PS97	Q7PS97 anopheles g
51	57.5	25.9	440	2	P90769	P90769 caenorhabdi
52	57.5	25.9	574	2	Q7R5J3	Q7R5J3 giardia lam
53	57.5	25.9	618	2	Q69ZA9	Q69ZA9 mus musculu
54	57.5	25.9	3550	2	Q66GT4	Q66GT4 rattus norv
55	57.5	25.9	7524	2	Q6P2E0	Q6P2E0 mus musculu
56	57	25.7	88	2	P94663	P94663 chlamydomphi
57	57	25.7	91	2	Q8H0Y6	Q8H0Y6 arabidopsis
58	57	25.7	92	2	Q8L7G7	Q8L7G7 arabidopsis
59	57	25.7	636	2	Q942D3	Q942D3 oryza sativ
60	57	25.7	722	1	SOA1_HUMAN	SOA1_HUMAN
61	56.5	25.5	87	2	Q9A1S8	Q9A1S8 chlamydomphi
62	56.5	25.5	371	2	Q72BJ2	Q72BJ2 desulfovibr
63	56	25.2	311	1	IBP2_CHICK	IBP2_CHICK
64	56	25.2	324	2	Q7RAW1	Q7RAW1 plasmodium
65	56	25.2	404	2	Q6IFW1	Q6IFW1 rattus norv
66	55.5	25.0	175	2	Q9PZR6	Q9PZR6 human cytom
67	55.5	25.0	389	2	Q97887	Q97887 bos taurus
68	55.5	25.0	461	1	PRTC_RAT	PRTC_RAT
69	55.5	25.0	514	2	Q6INT8	Q6INT8 rattus norv
70	55.5	25.0	717	2	Q8AXR0	Q8AXR0 xenopus lae
71	55.5	25.0	1637	2	Q9XSV8	Q9XSV8 bos taurus
72	55.5	25.0	5146	2	Q8SPM4	Q8SPM4 bos taurus
73	55	24.8	200	2	Q86YU6	Q86YU6 homo sapien
74	55	24.8	284	2	Q66T09	Q66T09 brachydanio
75	55	24.8	274	2	Q6W4T8	Q6W4T8 brachydanio
76	55	24.8	820	2	Q9FFK8	Q9FFK8 arabidopsis
77	54.5	24.5	85	1	CVPI_PIMHY	CVPI_PIMHY
78	54.5	24.5	123	1	D126_MACFA	D126_MACFA
79	54.5	24.5	131	2	Q9NB50	Q9NB50 macaca fasc
80	54.5	24.5	921	2	Q6CF14	Q6CF14 riftia pach
81	54.5	24.5	965	1	YNC3_YEAST	YNC3_YEAST
82	54	24.3	61	1	MT1A_BOVIN	MT1A_BOVIN
83	54	24.3	61	1	MT1B_SHEEP	MT1B_SHEEP
84	54	24.3	61	1	MT1C_SHEEP	MT1C_SHEEP
85	54	24.3	61	1	Q8MI14	Q8MI14 bos taurus
86	54	24.3	61	2	Q6R522	Q6R522 bos mutus g
87	54	24.3	61	2	Q6R522	Q6R522 aspergillus
88	54	24.3	819	2	Q672W0	Q672W0 caenorhabdi
89	54	24.3	1299	2	Q8MQ37	Q8MQ37 caenorhabdi
90	54	24.3	1587	1	LMG3_HUMAN	LMG3_HUMAN
91	54	24.3	2427	2	Q8MQ36	Q8MQ36
92	53.5	24.1	110	2	Q67WJ9	Q67WJ9 oryza sativ
93	53.5	24.1	277	2	Q9XZY1	Q9XZY1 leishmania
94	53.5	24.1	371	2	O18285	O18285 caenorhabdi
95	53.5	24.1	374	1	WIFI_XENLA	WIFI_XENLA
96	53.5	24.1	1859	2	Q7PS28	Q7PS28 xenopus lae
97	53.5	24.1	2585	2	Q23587	Q23587 anopheles g
98	53	23.9	61	1	MT1_BOVIN	MT1_BOVIN
99	53	23.9	119	2	Q9CVT5	Q9CVT5 mus musculu
100	53	23.9	140	2	O49628	O49628 arabidopsis

ALIGNMENTS

```

RESULT 1
ALB1_SOYBN
ID ALB1_SOYBN STANDARD; PRT; 119 AA.
AC Q39837; Q49854;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 precursor (Al1) [Contains: Albumin 1 chain b (Alb)
DE (Leguminin); Albumin 1 chain a (Ala)].
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagishiroe; TISSUE=Radicle;
RX MEDLINE=94357216; PubMed=8076638;
RA Watanabe Y., Barbaehov S.F., Komatsu S., Hemmings A.M., Miyagi M.,
RA Teunasaawa S., Hirano H.;
RT "A peptide that stimulates phosphorylation of the plant insulin-
RT binding protein. Isolation, primary structure and cDNA cloning.";
RL Eur. J. Biochem. 224:167-172(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagishiroe;
RA Tan J.Z., Lou C.F., Hirano H.;
RT "Analysis of leguminin gene in soybean cultivar (Glycine max) and
RT wild species (Glycine soja).";
RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).
RN [3]
RP REVISION TO 64.
RC STRAIN=cv. Miyagishiroe;
RA Hirano H.;
RL Submitted (JUN-2001) to Swiss-Prot.
RN [4]
RP STRUCTURE BY NMR OF 20-56, MUTAGENESIS OF ARG-35; VAL-48 AND PHE-50,
RP AND FUNCTION.
RC TISSUE=Radicle;
RX PubMed=12631285;
RA Yamazaki T., Takaoka M., Kato E., Hanada K., Sakita M., Sakata K.,
RA Nishuchi Y., Hirano H.;
RT "A possible physiological function and the tertiary structure of a 4-
RT kDa peptide in legumes.";
RL Eur. J. Biochem. 270:1269-1276(2003).
CC -!- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide.
CC -!- PTM: The C-terminal glycine may be removed from Alb.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D17396; BAA04219.1; -.
CC EMBL; AJ223037; CAA11040.1; -.
CC FIR; S48192; S48192.
CC 3D-structure; Plant toxin; Seed storage protein; Signal.
CC
CC SIGNAL 1 19 Albumin 1 chain b.
CC CHAIN 20 56 Potential.
CC PROPEP 57 64 Potential.
CC CHAIN 65 116 Albumin 1 chain a (Potential).
CC PROPEP 117 119 Potential.
CC DISULFID 22 39 By similarity.
CC DISULFID 26 41 By similarity.
CC DISULFID 34 51 By similarity.
CC SEQUENCE 119 AA; 12963 MW; 5E5457D8D09070CC CRC64;
CC
CC Query Match 97.3%; Score 216; DB 1; Length 119;
CC Best Local Similarity 97.3%; Pred. No. 1.3e-19;
CC Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC 1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
CC 20 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 56

```

```

FT MUTAGEN 35 35 R->A: No effect.
FT MUTAGEN 48 48 V->A: Decreased binding to globulin.
FT MUTAGEN 50 50 F->A: Decreased binding to globulin.
SQ SEQUENCE 119 AA; 13046 MW; A054491D7BE1AA70 CRC64;

Query Match 100.0%; Score 222; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
DB 20 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 56

RESULT 2
ALB1_GLYSO STANDARD; PRT; 119 AA.
ID ALB1_GLYSO
AC Q9ZQX0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 precursor (Al1) [Contains: Albumin 1 chain b (Alb)
DE (Leguminin); Albumin 1 chain a (Ala)].
OS Glycine soja (Wild soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3848;
RN [1]
RP SEQUENCE FROM N.A.
RA Tan J.Z., Lou C.F., Hirano H.;
RT "Analysis of leguminin gene in soybean cultivar (Glycine max) and
RT wild species (Glycine soja).";
RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).
CC -!- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity (By similarity).
CC -!- PTM: The C-terminal glycine may be removed from Alb.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ011935; CAA09880.2; -.
CC HSP; Q39837; IJ08.
CC Plant toxin; Seed storage protein; Signal.
CC
CC SIGNAL 1 19 Potential.
CC CHAIN 20 56 Albumin 1 chain b (By similarity).
CC PROPEP 57 64 Potential.
CC CHAIN 65 117 Albumin 1 chain a (Potential).
CC PROPEP 118 119 Potential.
CC DISULFID 22 39 By similarity.
CC DISULFID 26 41 By similarity.
CC DISULFID 34 51 By similarity.
CC SEQUENCE 119 AA; 12963 MW; EE5457D8D09070CC CRC64;
CC
CC Query Match 97.3%; Score 216; DB 1; Length 119;
CC Best Local Similarity 97.3%; Pred. No. 1.3e-19;
CC Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC 1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
CC 20 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 56

RESULT 3
Q7XZC3
ID Q7XZC3 PRELIMINARY; PRT; 100 AA.
AC Q7XZC3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

```


DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Albumin 1 precursor (Fragment).
GN Name=pai;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
RA Vallier A., Rabbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
DR EMBL; AJ574791; CAB00463.1; -.
DR HSSP; Q39837; IJU8.
KW Signal.
FT SIGNAL. 1 19 Potential.
FT CHAIN 20 56 Alb, albumin 1b.
FT CHAIN 65 >100 Ala, albumin 1a.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10982 MW; 281D9CE0F8B83611 CRC64;
Query Match 93.7%; Score 208; DB 2; Length 100;
Best Local Similarity 91.9%; Pred. No. 1.1e-18;
Matches 34; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPCRSRDCRCVPGLGVGFCIHPTG 37
DB 20 ADCNGACSPPEVPCRSRDCRCVPGLGVGFCIHPTG 56
RESULT 4
ALBI_PHAU
ID ALBI_PHAU STANDARD; PRT; 89 AA.
AC Q9FRT8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 precursor (Al) [Contains: Albumin 1 chain b (Alb)
DE (Leguminin); Albumin 1 chain a (Ala)] (Fragment).
GN Name=LEG;
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Blackmappe; TISSUE=Leaf;
RX PubMed=12631285;
RA Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita K.,
RA Nishitani Y., Hirano H.;
RT "A possible physiological function and the tertiary structure of a 4-
RT kDa peptide in legumes.";
RL Eur. J. Biochem. 270:1269-1276(2003).
CC -1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity (By similarity).
CC -1- PTM: The C-terminal glycine may be removed from Alb.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB052881; BAB19938.1; -.
DR HSSP; Q39837; IJU8.
KW Plant toxin; Seed storage protein; Signal.

FT NON_TER 1 1 Potential.
FT SIGNAL <1 1 Albumin 1 chain b (By similarity).
FT CHAIN 39 38 Potential.
FT PROPEP 39 46
FT CHAIN 47 >89 Albumin 1 chain a (Potential).
FT DISULFID 4 21 By similarity.
FT DISULFID 8 23 By similarity.
FT DISULFID 16 33 By similarity.
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 9711 MW; 4ADEB9797083135B CRC64;
Query Match 86.5%; Score 192; DB 1; Length 89;
Best Local Similarity 83.8%; Pred. No. 1.1e-16;
Matches 31; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPCRSRDCRCVPGLGVGFCIHPTG 37
DB 2 ADCNGACSPPEVPCRSRDCRCVPGLGVGFCIHPTG 38
RESULT 5
Q6A1C7
ID Q6A1C7 PRELIMINARY; PRT; 96 AA.
AC Q6A1C7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative albumin 1 precursor (Fragment).
GN Name=pai;
OS Vicia hirsuta.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Vicia.
OX NCBI_TaxID=3910;
RN [1]
RP SEQUENCE FROM N.A.
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Dupont G., Diol.O.,
RA Chesnel D., Rabbe Y.;
RT "Broad screening of the legume family for variability of insecticidal
RT activities and occurrence of seed albumin 1b toxins.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784951; CAH05251.1; -.
KW Signal.
FT SIGNAL. 1 26 Potential.
FT CHAIN 27 63 putative albumin 1b.
FT CHAIN 69 >96 putative albumin 1a.
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10546 MW; D8EF1B021A73DD7 CRC64;
Query Match 76.1%; Score 169; DB 2; Length 96;
Best Local Similarity 67.6%; Pred. No. 9.3e-14;
Matches 25; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPCRSRDCRCVPGLGVGFCIHPTG 37
DB 27 AECNGVCSPPPEVPCRSRDCRCVPGLGVGFCIHPTG 63
RESULT 6.
Q7XZC5
ID Q7XZC5 PRELIMINARY; PRT; 140 AA.
AC Q7XZC5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Albumin 1 precursor.

[illegible]

RA Jouvaneal L., Quillien L., Ferrasson E., Rahbe Y., Gueguen J.,
 RA Vovelle F.;
 RA "PALB, an insecticidal protein extracted from pea seeds (Pisum
 RA sativum): 1H-2-D NMR study and molecular modeling.";
 RL Biochemistry 42:11915-11923(2003).
 RN [4]
 RN FUNCTION.
 RX PubMed=12755698;
 RA Gressent F., Rahiou I., Rahbe Y.;
 RA "Characterization of a high-affinity binding site for the pea albumin
 RA lb entomotoxin in the weevil Sitophilus.";
 RL Eur. J. Biochem. 270:2429-2435(2003).
 CC -1- FUNCTION: PALB binds to basic 7S globulin (BG) and stimulates its
 CC phosphorylation activity. Involved in the signal transduction
 CC system to regulate the growth and differentiation as a hormone
 CC peptide (By similarity). Toxic to various insects through binding
 CC to a high affinity binding site in the insect gut.
 CC -1- PTM: The C-terminal glycine may be removed from PALB.
 CC -1- PTM: PALB displays a cysteine-knot (knottin) fold.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AJ574793; CAE00465.1; -.
 DR PDB; 1P8B; NMR; A=27-63; PH related.
 DR InterPro; IPR011036; PH related.
 KW 3D-structure; Direct protein sequencing; Plant toxin;
 KW Seed storage protein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 63 Albumin 1 F chain b.
 FT PROPEP 64 69 Potential.
 FT CHAIN 70 122 Albumin 1 F chain a.
 FT PROPEP 123 130 Potential.
 FT DISULFID 29 46
 FT DISULFID 33 48
 FT DISULFID 41 58
 SQ SEQUENCE 130 AA; 13913 MW; FD58E2D3C99D1644 CRC64;
 Query Match 69.4%; Score 154; DB 1; Length 130;
 Best Local Similarity 59.5%; Pred. No. 9.7e-12;
 Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 A D C G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 37
 DB 27 A S C N G V C S P F E M P P C G T S A C R C I P V G L V I G Y C R N P S G 63
 RESULT 17
 Q6ALD4
 ID Q6ALD4 PRELIMINARY; PRT; 98 AA.
 AC Q6ALD4
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative albumin 1 precursor (Fragment).
 GN Name=pal;
 OS Canavalia brasiliensis (Brazilian jack bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Canavalia.
 OX NCBI_TaxID=61861;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;
 RT "Gene structure, protein structure, and regulation of the synthesis of
 RT a sulfur-rich protein in pea seeds.";
 RL J. Biol. Chem. 261:11124-11130(1986).
 Query Match 69.4%; Score 151; DB 2; Length 99;
 Best Local Similarity 71.4%; Pred. No. 1.8e-11;
 Matches 25; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 3 C N G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 37
 DB 28 C S G A C F P F Q M P P C G S T D C R C V P W G L F V G Q C I D P I G 62
 RESULT 19
 Q7XZC2
 ID Q7XZC2 PRELIMINARY; PRT; 109 AA.

RN [2]
 RP SEQUENCE FROM N.A.
 RA Louis S., Delobel B., Gressent F., Rahiou I., Duport G., Diol O.,
 RA Chessel D., Rahbe Y.;
 RT "Broad screening of the legume family for variability of insecticidal
 RT activities and occurrence of seed albumin lb toxins.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ784944; CAH05244.1; -.
 KW Signal.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 62 putative albumin lb.
 FT CHAIN 71 >98 putative albumin la.
 FT NON_TER 98 98
 SQ SEQUENCE 98 AA; 10484 MW; B28B2E3919403D53 CRC64;
 Query Match 68.5%; Score 152; DB 2; Length 98;
 Best Local Similarity 67.6%; Pred. No. 1.3e-11;
 Matches 23; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 3 C N G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 36
 DB 28 C S G G C S P F F E M P P C G S D C R C I P W G L V A G Y C I N P T 61
 RESULT 18
 Q6ALD5
 ID Q6ALD5 PRELIMINARY; PRT; 99 AA.
 AC Q6ALD5
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative albumin 1 precursor (Fragment).
 GN Name=pal;
 OS Bituminaria bituminosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Psoraleae;
 OC Bituminaria.
 OX NCBI_TaxID=53836;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;
 RT "Gene structure, protein structure, and regulation of the synthesis of
 RT a sulfur-rich protein in pea seeds.";
 RL J. Biol. Chem. 261:11124-11130(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Louis S., Delobel B., Gressent F., Rahiou I., Duport G., Diol O.,
 RA Chessel D., Rahbe Y.;
 RT "Broad screening of the legume family for variability of insecticidal
 RT activities and occurrence of seed albumin lb toxins.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ784943; CAH05243.1; -.
 KW Signal.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 62 putative albumin lb.
 FT CHAIN 72 >99 putative albumin la.
 FT NON_TER 99 99
 SQ SEQUENCE 99 AA; 10767 MW; 27ACD82ABC4B2B92 CRC64;
 Query Match 68.0%; Score 151; DB 2; Length 99;
 Best Local Similarity 71.4%; Pred. No. 1.8e-11;
 Matches 25; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 3 C N G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 37
 DB 28 C S G A C F P F Q M P P C G S T D C R C V P W G L F V G Q C I D P I G 62
 RESULT 19
 Q7XZC2
 ID Q7XZC2 PRELIMINARY; PRT; 109 AA.

Query Match 61.9%; Score 137.5; DB 2; Length 101;
 Best Local Similarity 60.0%; Pred. No. 9.4e-10;
 Matches 24; Conservative 6; Mismatches 7; Indels 3; Gaps 2;

QY 1 ADGNG-ACSPRPVPC-RSRDCRCVPIGLFVGCIHPTG 37
 DB 26 ASCNGRDVCSPEMPFCDATNCRCIPWGLVGGCVHPSG 65

RESULT 21
 ALIC_PEA
 ID ALIC_PEA STANDARD; PRT: 130 AA.
 AC A62928; P08687; Q40999; Q7XZC0; Q9M3X4;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Albumin 1 C precursor (PAl C) (Psaalb015) [Contains: Albumin 1 C chain
 DE b (PAlb C) (Leginsulin C); Albumin 1 C chain a (PAla C)].
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Frisson; TISSUE=Seed;
 RA Louis S., Delobel B., Gressent F., Rahoui I., Quillien L.,
 RA Vallier A., Rabbe Y.;
 RA "Molecular and biological screening for insect-toxic seed albumins
 RT from four legume species.";
 RL Plant Sci. 167:705-714 (2004).
 RN [2]
 RP SEQUENCE OF 27-63, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
 RC TISSUE=Seed;
 RX MEDLINE=86278210; PubMed=3755437;
 RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;
 RA "Gene structure, protein structure, and regulation of the synthesis of
 RT a sulfur-rich protein in pea seeds.";
 RL J. Biol. Chem. 261:11124-11130 (1986).
 CC -I- FUNCTION: Palb binds to basic 7S globulin (BG) and stimulates its
 CC phosphorylation activity. Involved in the signal transduction
 CC system to regulate the growth and differentiation as a hormone
 CC peptide. Toxic to various insects through binding to a high
 CC affinity binding site in the insect gut (by similarity).
 CC -I- TISSUE SPECIFICITY: Major component of both the cotyledons and
 CC embryonic axes of mature seeds.
 CC -I- DEVELOPMENTAL STAGE: Increasing expression during seed development
 CC followed by a rapid degradation during the first days of seed
 CC germination.
 CC -I- PTM: The C-terminal glycine may be removed from Palb.
 CC -I- MISCELLANEOUS: The protein sequenced in Ref.2 was probably a
 CC mixture of the products of genes C and D, Palb being of C origin
 CC while Pala is of D origin.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; AJ574796; CAE00468.1; --
 DR InterPro; IPR011036; PH_related.
 KW Direct protein sequencing; Plant toxin; Seed storage protein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 63 Albumin 1 C chain b.
 FT PROPEP 64 69
 FT CHAIN 70 122 Albumin 1 C chain a.
 FT PROPEP 123 130 Potential.
 FT DISULFID 29 46 By similarity.
 FT DISULFID 33 48 By similarity.

	FT	DISULFID	41	58	By similarity.	
	FT	CONFLICT	60	N -> H (in Ref. 2).		
	SQ	SEQUENCE	130 AA;	13912 MW;	12C8EA2B8300A723 CRC64;	
		Query Match	61.3%;	Score 136;	DB 1;	Length 130;
		Best Local Similarity	60.0%;	Pred. No. 1.8e-09;		
		Matches	21;	Conservative	5;	Mismatches 9;
						Indels 0;
						Gaps 0;
	QY	3 CNGACSPFEVPPCRSDRCVPICGLFVGFCIHPTG	37			
		:: :	:	:	:	:
	Dd	29 CNGVCSPFDIPPCSGPLCRCIPAGLVIGNCRNPG	63			
		:: :	:	:	:	:
	RESULT 22 .					
	Q6AID2	ID Q6AID2 PRELIMINARY;	PRT;	98 AA.		
	AC Q6ALD2	PRELIMINARY;	PRT;	98 AA.		
	DT 25-OCT-2004	(TREMELrel. 28, Created)				
	DT 25-OCT-2004	(TREMELrel. 28, Last sequence update)				
	DE DE Putative albumin 1 precursor (Fragment).					
	GN Names=pal;					
	OS Melilotus alba (White sweet clover).					
	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;					
	OX eurosoids I; Fabales; Fabaaceae; Papilionoideae; Trifolieae; Melilotus.					
	NCBI_TaxID=47082;					
	[1]					
	RN RN SEQUENCE FROM N.A.					
	RP Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,					
	RA Blagrove R.J., Kortt A.A., Inglis A.S.;					
	RT "Gene structure, protein structure, and regulation of the synthesis of					
	a sulfur-rich protein in pea seeds."					
	J. Biol. Chem. 261:11124-11130(1986).					
	[2]					
	RN RN SEQUENCE FROM N.A.					
	RP Louis S., Delobel B., Gressent F., Rahiou I., Dupont G., Diol O.,					
	RA Chessel D., Rabhe Y.;					
	RT "Broad screening of the legume family for variability of insecticidal					
	activities and occurrence of seed albumin lb toxins."					
	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.					
	DR EMBL; AJ784946; CAH05246.1; -.					
	KW SIGNAL.					
	FT FT SIGNAL					
	FT CHAIN	1	26	Potential.		
	FT CHAIN	27	63	putative albumin lb.		
	FT CHAIN	71	>98	putative albumin la.		
	FT NON_TER	98	98			
	SQ SEQUENCE	98 AA;	10691 MW;	EF28472D809499AB CRC64;		
	Query Match	57.7%;	Score 128;	DB 2;	Length 98;	
	Best Local Similarity	54.3%;	Pred. No. 1.4e-08;			
	Matches	19;	Conservative	7;	Mismatches 9;	Indels 0;
						Gaps 0;
	QY	2 DCNGACSPFEVPPCRSDRCVPICGLFVGFCIHPT	36			
		:: :: :	:	:	:	:
	Dd	28 ECSGCSCSPEMPCCRSSCRCPVLLGGNCVDPS	62			
		:: :	:	:	:	:
	RESULT 23					
	ALBU_LUPAN	ID ALBU_LUPAN STANDARD;	PRT;	81 AA.		
	AC Q96474;					
	DT 16-OCT-2001	(Rel. 40, Created)				
	DT 16-OCT-2001	(Rel. 40, Last sequence update)				
	DE DE Putative albumin 1 precursor (Al)					
	DE Albinin i precursor (Al)					
	(Legninsulin); Albumin i chain a (Ala)]					
	Name=LEG1;					
	OS Lupinus angustifolius (Narrow-leaved blue lupine).					
	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;					
	OX eurosoids I; Fabales; Fabaaceae; Papilionoideae; Genisteae; Lupinus.					
	NCBI TaxID=3871;					

[1]
SEQUENCE FROM N.A.
STRAIN=cv. Unicorn;
MEDLINE=97390686; PubMed=9247543; DOI=10.1023/A:1005868105651;
RX lgloutz S.C., Knittel N., Lin J.M., Sterle S., Gayler K.R.;
RT "transcription of genes for conglutin gamma and a legninsulin-like
protein in narrow-leaved lupin.";
RL Plant Mol. Biol. 34:613-627(1997).
CC -|- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
phosphorylation activity (By similarity).
CC -|- PTM: Three disulfide bonds are probably present.
CC -|- PTM: The C-terminal glycine may be removed from Alb.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)

CC EMBL; U74383; AAC49786.1; -.
DR HSSP; Q39837; LUU8.
KW Plant toxin; Seed storage protein.
RN NON_TER 1
FT CHAIN <1 26 Albumin i chain b (By similarity).
FT PROPEP 27 34 Potential.
FT CHAIN 35 >81 Albumin i chain a (Potential).
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 8908 MW; 70014D8E9BBF5439 CRC64;

Query Match 56.3%; Score 125; DB 1; Length 81;
Best Local Similarity 80.8%; Pred. No. 2.9e-08;
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 VPPCSRDCRCVPICGLFVGFCIHPTG 37
:|||::|||:
Db 1 IPPSRSDRCVPITLVIGFCIHPTG 26
:|||::|||:

RESULT 24
Q6AID1 ID Q6AID1 PRELIMINARY; PRT; 101 AA.
AC Q6

[illegible]


```

FT NON TER 101 101
SQ SEQUENCE 101 AA; 11068 MW; 26ECD6B970BD10E2 CRC64;

Query Match      56.1%; Score 124.5; DB 2; Length 101;
Best Local Similarity 55.3%; Pred. No. 4.1e-08;
Matches 21; Conservative 8; Mismatches 6; Indels 3; Gaps 2;

QY 3 CNGA--CSPEVPDC-RSRDCRCVPICGLFVGFCIHPTG 37
   ||| ||||| ||||| :|||:| :|||:| :|||:|
Db 27 CNGRDWCSPFMPGCGAQCRCIPVVLVGGYCRHPSG 64

RESULT 25
Q7XZC4
ID Q7XZC4 PRELIMINARY; PRT; 142 AA.
AC Q7XZC4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Albumin 1 precursor.
GN Name=pal;
OS Medicago truncatula (Barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
RA Vallier A., Rabbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714 (2004).
DR EMBL; AJ574790; CAB00462.1; -.
DR HSSP; Q39837; 1JU8.
KW Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 142 albumin 1.
SQ SEQUENCE 142 AA; 15727 MW; F35A1A5A9EDA9E2F CRC64;

Query Match      54.5%; Score 121; DB 2; Length 142;
Best Local Similarity 54.3%; Pred. No. 1.6e-07;
Matches 19; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 2 DCGACSPFVEVPPCRSRDCRCVPICGLFVGFCIHPT 36
   ||| ||||| ||||| ||||| :|||:| :|||:| :|||:|
Db 29 DCGICSPFEMPPCPSSSCRCIPVILICGNVDP 63

```

Search completed: March 28, 2005, 09:00:08

Job time : 86 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:50:15 ; Search time 23.5 Seconds
(without alignments)
151.490 Million cell updates/sec

Title: US-09-674-496d-8

Perfect score: 222

Sequence: 1 ADCNGACSPFPPCRSDRCVPIGLFVGFCIRPTG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.79.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	119	2	S48192
2	155	69.8	130	2	A25014
3	63	28.4	3075	2	S14458
4	62.5	28.2	379	2	A59180
5	61.5	27.7	1847	2	T18308
6	59	26.6	3084	1	MMMSA
7	57.5	25.9	87	2	A39439
8	57.5	25.9	1018	2	T19693
9	57	25.7	88	2	JC5203
10	55.5	25.0	461	1	S18994
11	54.5	24.5	965	2	S62935
12	54	24.3	61	1	SMB02
13	54	24.3	61	2	S00808
14	54	24.3	61	2	S00810
15	54	24.3	61	2	S00809
16	54	24.3	2195	2	T34264
17	53.5	24.1	371	2	T27643
18	53.5	24.1	1023	2	T30257
19	53.5	24.1	3507	2	T34513
20	53	23.9	61	2	A23889
21	53	23.9	140	2	T04904
22	53	23.9	295	2	A44984
23	53	23.9	3229	2	S27852
24	53	23.9	3566	1	A40701
25	53	23.9	4006	2	T09070
26	53	23.9	13288	2	T03099
27	52	23.4	130	1	K8SHA
28	52	23.4	435	2	I54182
29	52	23.4	582	2	T34538

30	52	23.4	820	2	G86246	hypothetical prote
31	51.5	23.2	340	2	T20148	probable cysteine
32	51	23.0	31	2	A59440	neurotoxin Bmk37 -
33	51	23.0	161	2	AD3462	hypothetical prote
34	51	23.0	174	2	B48454	cathepsin B-like c
35	51	23.0	304	2	T24703	hypothetical prote
36	51	23.0	561	1	A44128	(N-acetylneuraminy
37	51	23.0	593	1	GYHU	granulin precursor
38	51	23.0	1535	2	S46224	peroxidase - frui
39	50.5	22.7	62	2	S35098	trypsin inhibitor
40	50.5	22.7	90	2	B86560	9 kDa-Cysteine-ric
41	50.5	22.7	90	2	A72064	cysteine rich oute
42	50.5	22.7	1101	2	T16840	hypothetical prote
43	50.5	22.7	1104	2	T38869	transcription fact
44	50.5	22.7	1110	1	B42544	G2-G1 polyprotein
45	50.5	22.7	1188	2	D86236	protein F14N23.5 [
46	50	22.5	31	2	A59357	neurotoxin Bmk KTX
47	50	22.5	31	2	A59321	protein BmSKTx2 [i
48	50	22.5	48	1	A44664	omega-agatoxin IVB
49	50	22.5	61	2	T48173	metallothionein II
50	50	22.5	77	2	AD3531	hypothetical prote
51	50	22.5	273	2	B83489	probable binding p
52	50	22.5	404	2	JS0073	keratin, 47.6K typ
53	50	22.5	408	1	QRHUBE	beta-3-adrenergic
54	50	22.5	414	1	QRHUB3	beta-3-adrenergic
55	50	22.5	473	2	A56175	adhesive plaque pr
56	50	22.5	860	2	A96717	unknown protein, 4
57	49.5	22.3	57	2	A57537	guamerin - Korean
58	49.5	22.3	238	2	JQ2393	V protein - Newcas
59	49.5	22.3	1373	2	JS0095	gastric mucin MUC5
60	49.5	22.3	1639	1	MMFPB2	laminin gamma-1 Ch
61	49	22.1	61	1	MMMS2	metallothionein II
62	49	22.1	61	2	I57572	metallothionein II
63	49	22.1	325	2	JN0148	necdin, brain - mo
64	49	22.1	418	2	G02953	beta-3-adrenergic
65	49	22.1	475	2	D88451	protein K10D2.2 [i
66	49	22.1	1124	1	I58388	protein-tyrosine k
67	49	22.1	1239	2	T13809	probable disintegr
68	49	22.1	1245	1	MMGND	nidogen precursor
69	49	22.1	1506	2	T30886	integumentary muc
70	49	22.1	1574	2	T13954	MEGF6 protein - ra
71	49	22.1	3770	2	A40889	delta-(L-alpha-ami
72	48.5	21.8	63	2	S07127	chymotrypsin/elast
73	48.5	21.8	245	1	A47539	homeotic protein g
74	48.5	21.8	252	1	A54677	homeotic protein g
75	48.5	21.8	256	1	A42768	homeotic nicotinat
76	48.5	21.8	258	2	B36914	hypothetical prote
77	48.5	21.8	650	2	H81708	nucleotide diphosp
78	48.5	21.8	905	1	A27410	hypothetical prote
79	48.5	21.8	1106	2	T44598	gene shuttle craft
80	48.5	21.8	1106	2	T13938	trach
81	48.5	21.8	1321	2	JE0352	major blood-stage
82	48.5	21.8	1726	2	A39401	probable vitellog
83	48.5	21.8	1751	2	A45604	metallothionein -
84	48.5	21.8	1984	2	T13171	metallothionein -
85	48	21.6	43	2	S33382	metallothionein -
86	48	21.6	43	2	S18173	metallothionein -
87	48	21.6	43	2	S18174	metallothionein -
88	48	21.6	63	2	A34958	metallothionein -
89	48	21.6	63	2	S33381	metallothionein -
90	48	21.6	63	2	A34620	metallothionein -
91	48	21.6	63	2	C34620	metallothionein -
92	48	21.6	107	4	S57707	hypothetical prote
93	48	21.6	152	2	D95961	hypothetical prote
94	48	21.6	202	2	T50635	glutamate COA-tr
95	48	21.6	266	2	S51052	hypothetical prote
96	48	21.6	325	2	H71271	hypothetical prote
97	48	21.6	374	2	T18602	hypothetical prote
98	48	21.6	375	2	T16248	hypothetical prote
99	48	21.6	457	2	T46332	hypothetical prote
100	48	21.6	480	2	F84454	hypothetical prote

ALIGNMENTS

RESULT 1

S48192
insulin-like growth factor S11 precursor - soybean
N;Alternate names: leguminin
C;Species: Glycine max (soybean)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S48192; PNM0116
R;Watanabe, Y.; Barbashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunasawa, S.;
Eur. J. Biochem. 224, 167-172, 1994
A;Title: A peptide that stimulates phosphorylation of the plant insulin-binding protein.
A;Reference number: S48192; MUID:94357216; PMID:8076638
A;Accession: S48192
A;Molecule type: mRNA; protein
A;Residues: 1-119 <WAT>
A;Cross-references: UNIPROT:Q99837; GB:D17396; NID:G498167; PIDN:BAA04219.1; PID:G498168
R;Barbashov, S.F.; Egorov, T.A.
Mol. Biol. (Mosk.) 24, 953-961, 1990
A;Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cell g
A;Reference number: PNM0115; MUID:91066897; PMID:2250683
A;Accession: PNM0116
A;Molecule type: protein
A;Residues: 20-30,'M',32-39 <BAR>
F;1-19/Domain: propeptide #status predicted <PRO>
F;20-56/Product: insulin-like growth factor S11 #status experimental <MAT>

Query Match 100.0%; Score 222; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPPCRSDRCRCVPGLFVGFCIHPTG 37
Db 20 ADCNGACSPPEVPPCRSDRCRCVPGLFVGFCIHPTG 56

RESULT 2

A25014
albumin precursor - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 16-Aug-1998 #sequence_revision 16-Aug-1998 #text_change 09-Jul-2004
C;Accession: A25014
R;Higgins, T.J.V.; Chandle, P.M.; Randall, P.J.; Spencer, D.; Beach, L.R.; Blagrove, R.
J. Biol. Chem. 261, 11124-11130, 1986
A;Title: Gene structure, protein structure, and regulation of the synthesis of a sulfur-
A;Reference number: A25014; MUID:86278210; PMID:3755437
A;Accession: A25014
A;Molecule type: DNA
A;Residues: 1-130 <HIG>
A;Cross-references: UNIPROT:P08687; GB:M13709; NID:G169024; PIDN:AAA33638.1; PID:G169025
C;Genetics:
A;Introns: 17/1
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-130/Product: albumin #status predicted <MAT>

Query Match 69.8%; Score 155; DB 2; Length 130;
Best Local Similarity 62.2%; Pred. No. 1.3e-11;
Matches 23; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPPCRSDRCRCVPGLFVGFCIHPTG 37
Db 27 ASCNGVCSPEMPFCGTACRCIPVGLVVGCRNPSG 63

RESULT 3

S14458
laminin alpha-1 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; A34961
R;Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991

A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: S14458; MUID:91333420; PMID:1714537
A;Accession: S14458
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3075 <HAA>
A;Cross-references: UNIPROT:P25391
R;Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A;Title: Primary structure of the human laminin A chain. Limited expression in human tis
A;Reference number: S14663; MUID:91264789; PMID:2049067
A;Accession: S14663
A;Molecule type: mRNA
A;Residues: 1-227,'FE',230-251,'MLP',255-418,'E',420-518,'L',520-1022,'V',1024-1074,'V',1
A;Cross-references: EMBL:X58531; NID:G34225; PIDN:CAA41418.1; PID:G34226
R;Olsen, D.; Nagayoshi, T.; Razio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T.
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: A34961
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP', <OLS>
A;Note: the authors translated the codon AGA for residue 2692 as Pro
C;Genetics:
A;Gene: GDB:LAMAL1; LAMA
A;Cross-references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.22
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hom
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F;18-269/Domain: VI <DOM6>
F;270-516/Domain: V <DOM5>
F;270-324/Domain: laminin-type EGF-like homology <LE1>
F;327-394/Domain: laminin-type EGF-like homology <LE2>
F;397-451/Domain: laminin-type EGF-like homology <LE3>
F;454-500/Domain: laminin-type EGF-like homology <LE4>
F;503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F;517-708/Domain: IIV <DO4B>
F;709-1159/Domain: IIIB <DO3B>
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F;742-788/Domain: laminin-type EGF-like homology <LE7>
F;791-846/Domain: laminin-type EGF-like homology <LE8>
F;849-899/Domain: laminin-type EGF-like homology <LE9>
F;902-948/Domain: laminin-type EGF-like homology <LE10>
F;951-995/Domain: laminin-type EGF-like homology <LE11>
F;998-1041/Domain: laminin-type EGF-like homology <LE12>
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>
F;1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1160-1361/Domain: IVA <DO4A>
F;1362-1553/Domain: IIIfa <DO3A>
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1403-1449/Domain: laminin-type EGF-like homology <LE18>
F;1452-1506/Domain: laminin-type EGF-like homology <LE19>
F;1509-1553/Domain: laminin-type EGF-like homology <LE20>
F;1554-2125/Domain: I/II, heptad repeats <DOM2>
F;2116-2120/Region: cell adhesion #status predicted
F;2126-3075/Domain: G <DOMG>
F;2142-2300/Domain: laminin G repeat homology <LG1>
F;2329-2484/Domain: laminin G repeat homology <LG2>
F;2510-2676/Domain: laminin G repeat homology <LG3>
F;2534-2536/Region: cell attachment (R-G-D) motif
F;2739-2888/Domain: laminin G repeat homology <LG4>
F;2916-3073/Domain: laminin G repeat homology <LG5>
F;38,164,555,665,763,801,838,926,1045,1407,1579,1596,1678,1689,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F;297-305/Disulfide bonds: #status predicted

Query Match 28.4%; Score 63; DB 2; Length 3075;
Best Local Similarity 46.2%; Pred. No. 15;


```

QY      2 DC-NGACSPFEVPPC-RSRDRCVPIGLFVGFCIHPTG 37
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      25 DCCFEDCAPKPCNPGNKDKGCSGCVYTFSCKPCG 63

      submitted to the EMBL Data Library, December 1996
      A;Reference number: Z19165
      A;Accession: T19693
      A;Status: preliminary; translated from GB/EMBL/DBJ
      A;Molecule type: DNA
      A;Residues: 1-1018 <WIL>
      A;Cross-references: UNIPROT:P90769; EMBL:Z83220; PIDN:CAB05700.1; GSPDB:GNO
      A;Experimental source: clone C34B7
      C;Genetics:
      A;Gene: CESP:C34B7.1
      A;Map position: 1
      A;Introns: 78/1; 149/1; 177/1; 245/1; 311/2; 361/2; 387/3; 415/2; 44
      Query Match      25.9%; Score 57.5; DB 2; Length 1018;
      Best Local Similarity 32.4%; Pred. No. 29;
      Matches 12; Conservative 2; Mismatches 16; Indels 7; Gaps

QY      3 CNGACSPFEVPPCSR-----DCRCVPIGLFVGFC 32
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      133 CNNYCNPGTPIPIQORPLVRCYDCSSSDSCFTGSC 169

RESULT 9
JC5203
outer membrane protein 3 precursor - Chlamydophila psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 31-Mar-2000
C;Accession: JC5203
R;Hsia, R.; Bavoil, P.M.
Gene 176, 155-162, 1996
A;Title: Sequence analysis of the omp2 region of Chlamydia psittaci strain
A;Reference number: JC5203; MUID:97075924; PMID:8918247
A;Accession: JC5203
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <HSL>
A;Cross-references: GB:U41759; NID:gl783376; PIDN:AAB41142.1; PID:gl783381
A;Experimental source: strain GPIC
C;Genetics:
A;Gene: omp3
F;1-19/Domain: signal sequence #status predicted <SIG>

      Query Match      25.7%; Score 57; DB 2; Length 88;
      Best Local Similarity 32.5%; Pred. No. 4.9;
      Matches 13; Conservative 3; Mismatches 20; Indels 4; Gaps

QY      2 DC-NGACSPFEVPPCR--SRDRCVPIGLFVGFCIHPTG 37
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      25 DCCFEDCAPKSCNFCNVFKDGCSCGSYTFSCKPCG 64

RESULT 10
S18994
protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
R;Okatuj, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Description: The EMBL Data Library, February 1992
A;Description: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S18994

```

A;Accession: S18994
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OKA>
A;Cross-references: UNIPROT:P31394; EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S24312; MUID:92329550; PMID:1627650
A;Accession: S24312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OKA2>
A;Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;1-32/Domain: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F;27-85/Domain: Gla domain homology <GLA>
F;33-42/Domain: propeptide homology predicted <PRO>
F;43-461/Product: protein C #status predicted <PRC>
F;91-130/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
F;213-445/Domain: trypsin homology <TRY>
F;47, 48, 55, 57, 60, 61, 66, 67, 70, 76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat
F;215,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted
F;254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 25.0%; Score 55.5; DB 1; Length 461;
Best Local Similarity 42.3%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

Qy 2 DC---NGACSPFVEVPPCRSDRCRCP 24
||| ||| : : : ||| |||
Db 138 DCRVNGGCVHYCLEETRRRCRCAP 163

RESULT 11
S62935
hypothetical protein YNL023c - Yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N2812
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S62935; S62945
R;Andre, B.; Iraqi Housaini, I.; Urrestarazu, L.A.; Vissers, S.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62920
A;Accession: S62935
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-965 <AND>
A;Cross-references: UNIPROT:P53971; EMBL:Z71299; NID:G1301854; PID:e239870; PID:G1301855
A;Experimental source: strain S288C
R;Duisterhoft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S62945
A;Molecule type: DNA
A;Residues: 1-965 <DUE>
A;Cross-references: EMBL:Z71299; NID:G1301854; PID:e239870; PID:G1301855; MIPS:YNL023c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:FAP1
A;Cross-references: SGD:S0004968
A;Map position: 14L

Query Match 24.5%; Score 54.5; DB 2; Length 965;
Best Local Similarity 30.4%; Pred. No. 64;
Matches 14; Conservative 2; Mismatches 17; Indels 13; Gaps 2;

Qy 3 CNGACSPFVEVPPCRSD-----CRC-----VPIGLFVGCFCIHP 35
||| ||| : : : ||| |||
Db 473 CQRKCHFKCPCLCSDSNLDVCPGNTVWPAPVRCGKLPCTCNHP 518

RESULT 12
SMB02
metallothionein II - bovine
N;Alternate names: MT-II
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A03279
R;Winge, D.R.; Gray, W.R.; Zelazowski, A.; Garvey, J.S.
Arch. Biochem. Biophys. 245, 254-262, 1986
A;Title: Sequence and antigenicity of calf metallothionein II.
A;Reference number: A03279; MUID:86129456; PMID:3947100
A;Accession: A03279
A;Molecule type: protein
A;Residues: 1-61 <WIN>
A;Cross-references: UNIPROT:P04356
A;Experimental source: calf liver
A;Note: 49-Ile was also found
C;Comment: The vertebrate metallothioneins contain two metal-binding domains. Clusters of
C;Superfamily: metallothionein
C;Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster
F;1-29/Domain: beta <NH2>
F;30-61/Domain: alpha <MLP>
F;1/Modified site: acetylated amino end (Met) #status experimental
F;5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F;33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre-

RESULT 19
T34513
hypothetical protein ZK783.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34513
R;Favella, A.; Vaudin, M.
submitted to the EMBL Data Library, August 1994
A;Description: The sequence of C. elegans cosmid ZK783.
A;Reference number: Z21536
A;Accession: T34513
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3507 <FAV>
A;Cross-references: UNIPROT:Q23587; EMBL:U13646; PIDN:AAC24418.1; GSPDB:GNO0021; CESP:ZK783
A;Experimental source: strain Bristol N2; clone ZK783
C;Genetics:
A;Gene: CESP:ZK783.1
A;Map position: 3
A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 3504/1
Query Match 24.1%; Score 53.5; DB 2; Length 3507;
Best Local Similarity 42.3%; Pred. No. 2.3e+02;
Matches 11; Conservative 5; Mismatches 5; Indels 5; Gaps 2;
QY 2 DC---NGACSPFEVPPCRSRDCRCPV 24
Db 3028 DCVLRDLCSPEAV--CONRRCCQLP 3051
RESULT 20
A23889
metallothionein 1 - bovine (tentative sequence)
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23889
R;Munger, K.; Germann, U.A.; Beltracchi, M.; Niedermann, D.; Baitella-Eberle, G.; Kagi, J. Biol. Chem. 260, 10032-10038, 1985
A;Title: (Cu,Zn)-metallothioneins from fetal bovine liver. Chemical and spectroscopic properties
A;Reference number: A92490; MUID:85261416; PMID:4019500
A;Accession: A23889
A;Molecule type: protein
A;Residues: 1-61 <MUN>
A;Cross-references: UNIPROT:P59280
C;Superfamily: metallothionein
Query Match 23.9%; Score 53; DB 2; Length 61;
Best Local Similarity 34.6%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 12; Indels 2; Gaps 1;
QY 3 CNGA--CSPFEVPPCRSRDCRCPVIG 26
Db 15 CAGSCCKACRCPSCKKSCCSCPVG 40
RESULT 21
T04904
hypothetical protein T10114.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04904
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15389
A;Accession: T04904
A;Molecule type: DNA
A;Residues: 1-140 <BRV>
A;Cross-references: UNIPROT:O49628; EMBL:AL021712
A;Experimental source: cultivar Columbia; BAC clone T10114
C;Genetics:

A;Map position: 4
A;Introns: 26/1; 73/1
A;Note: T10114.60
Query Match 23.9%; Score 53; DB 2; Length 140;
Best Local Similarity 31.2%; Pred. No. 21;
Matches 10; Conservative 6; Mismatches 6; Indels 10; Gaps 2;
QY 5 GACSPFE-----VPPCRSRDC-----RCVPIG 26
Db 38 GECNSYEKSKSTCIPECKQLDSKFGRCIDPVG 69
RESULT 22
A44984
collagen - nematode (Haemonchus contortus)
C;Species: Haemonchus contortus
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 15-Sep-2003
C;Accession: A44984
R;Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N.
Mol. Biochem. Parasitol. 37, 73-86, 1989
A;Title: Cuticle collagen genes of Haemonchus contortus and Caenorhabditis elegans are h
A;Reference number: A44984; MUID:90136718; PMID:2615789
A;Accession: A44984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <SHA>
A;Cross-references: GB:J04670
Query Match 23.9%; Score 53; DB 2; Length 295;
Best Local Similarity 39.1%; Pred. No. 38;
Matches 9; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
QY 4 NGACSPFEVPPCRSRDCRCPVIG 26
Db 130 DGSCEPVSIPPC--AECPAGPPG 150
RESULT 23
S27852
probable cell-surface protein (cysteine-rich repeat motif) - Trypanosoma cruzi
N;Alternate names: hypothetical protein DGF-1
C;Species: Trypanosoma cruzi
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A48450; S27852
R;Wincker, P.; Murto-Dovalles, A.C.; Goldenberg, S.
Mol. Biochem. Parasitol. 55, 217-220, 1992
A;Title: Nucleotide sequence of a representative member of a Trypanosoma cruzi dispersed
A;Reference number: A48450; MUID:93083053; PMID:1435871
A;Accession: A48450
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-3229 <W12>
A;Cross-references: UNIPROT:Q26912; EMBL:M90534; NID:g162051; PID:g162052
A;Note: sequence extracted from NCBI backbone (NCBIP:118407)
C;Superfamily: Trypanosoma cruzi probable cell-surface protein (cysteine-rich repeat mot
Query Match 23.9%; Score 53; DB 2; Length 3229;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 ACSPFEPVPPCRSR 18
Db 260 ACLPFDVPPARPR 272
RESULT 24
A40701
tenascin-X precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A40701; A33725; C42175
R;Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.

J. Cell Biol. 122, 265-278, 1993
A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene
A;Reference number: A40701; MUID:93300909; PMID:7686164
A;Accession: A40701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3566 <BRI>
A;Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; EMBL:X71937
R;Morel, Y.; Brietow, J.; Gitelman, S.E.; Miller, W.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989
A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/
A;Reference number: A33725; MUID:89367293; PMID:2475872
A;Accession: A33725
A;Molecule type: mRNA
A;Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>
A;Cross-references: GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:g183070
R;Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.
Genomics 12, 485-491, 1992
A;Title: Cluster of fibronectin type III repeats found in the human major histocompatibility
enascin.
A;Reference number: A42175; MUID:92217969; PMID:1373119
A;Accession: C42175
A;Molecule type: DNA
A;Residues: 1849-1936 <MAT>
A;Experimental source: clone 3.9kF3-1
A;Note: sequence extracted from NCBI backbone (NCBIP:95694)
C;Genetics:
A;Gene: GDB:TNXA; D6S103E; TNX; XA; XB
A;Cross-references: GDB:568487; OMIM:600261
A;Map position: 9p21.3-9p21.3
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: extracellular matrix; glycoprotein
F;435-461/Domain: EGF homology <EGF>
F;748-828/Domain: fibronectin type III repeat homology <3F1>
F;829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>
F;873-953/Domain: fibronectin type III repeat homology <3F3>
F;975-1055/Domain: fibronectin type III repeat homology <3F4>
F;1078-1158/Domain: fibronectin type III repeat homology <3F5>
F;1167-1247/Domain: fibronectin type III repeat homology <3F6>
F;1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7>
F;1323-1403/Domain: fibronectin type III repeat homology <3F8>
F;1412-1492/Domain: fibronectin type III repeat homology <3F9>
F;1510-1590/Domain: fibronectin type III repeat homology <3F10>
F;1618-1676/Domain: fibronectin type III repeat homology #status atypical <3F11>
F;1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12>
F;1751-1831/Domain: fibronectin type III repeat homology <3F13>
F;1849-1929/Domain: fibronectin type III repeat homology <3F14>
F;1955-2035/Domain: fibronectin type III repeat homology <3F15>
F;2061-2141/Domain: fibronectin type III repeat homology <3F16>
F;2167-2246/Domain: fibronectin type III repeat homology <3F17>
F;2274-2354/Domain: fibronectin type III repeat homology <3F18>
F;2382-2462/Domain: fibronectin type III repeat homology <3F19>
F;2488-2568/Domain: fibronectin type III repeat homology <3F20>
F;2584-2664/Domain: fibronectin type III repeat homology <3F21>
F;2677-2757/Domain: fibronectin type III repeat homology <3F22>
F;2771-2851/Domain: fibronectin type III repeat homology <3F23>
F;2878-2958/Domain: fibronectin type III repeat homology <3F24>
F;2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25>
F;3078-3159/Domain: fibronectin type III repeat homology <3F26>
F;3167-3247/Domain: fibronectin type III repeat homology <3F27>
F;3255-3334/Domain: fibronectin type III repeat homology <3F28>
F;3349-3557/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 23.9%; Score 53; DB 1; Length 3566;
Best Local Similarity 47.6%; Pred. No. 2.7e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 3 CNGACSPFEVPCRSRDCRCV 23
DB 688 CPGGCGPREL--CRAGQCVCV 706

RESULT 25

T09070

probable tenascin X - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09070
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Loretz, C.; Sci
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4006 <ROW>
C;Cross-references: UNIPROT:O35452; EMBL:AF030001; NID:g2564945; PID:g2564958
C;Genetics:
A;Gene: TNX
A;Map position: 17
A;Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: extracellular matrix
F;422-448/Domain: EGF homology <EGF>
F;826-906/Domain: fibronectin type III repeat homology <3FR>
F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 23.9%; Score 53; DB 2; Length 4006;
Best Local Similarity 47.6%; Pred. No. 3e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 3 CNGACSPFEVPCRSRDCRCV 23
DB 675 CPGGCGPREL--CRAGQCVCV 693

Search completed: March 28, 2005, 09:01:07
Job time : 25.5 secs


```

; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 653
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-653

Query Match          30.2%; Score 67; DB 9; Length 158;
Best Local Similarity 32.6%; Pred. No. 4;
Matches 14; Conservative 5; Mismatches 14; Indels 10; Gaps 1;

Qy      5  GACSPPEVPPCRSRDCRCVPIGLFGVGFPC-----IHPGTG 37
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      96  GGQQPSQPPARASQCPQPSLQLFLGFCSQLVGFPTCALHPRG 138

RESULT 7
US-09-938-275-5
; Sequence 5, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: OF Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3075
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P35391
; DATABASE ENTRY DATE: 1992-05-01
US-09-938-275-5

Query Match          28.4%; Score 63; DB 9; Length 3075;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy      8  SPPEVPPCRSRDCRCVPIGLFGVGFCI 33
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      387  SPYEDEFPC--RPCNCDPVGSLSSVCI 410

RESULT 8
US-10-437-963-187490
; Sequence 187490, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187490
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

```

OTHER INFORMATION: Clone ID: PAT_MRT4530_84188C.1.pcp
US-10-437-963-187490

Query Match	28.2%	Score 62.5;	DB 16;	Length 77;
Best Local Similarity	46.2%	Pred. No. 7;		
Matches 12; Conservative	0;	Mismatches 9;	Indels 5;	Gaps 1;

Qy 2 DCNGA-----CSPFEVPPCRSRDCRC 22

Db 50 DCKAAGLTAVCPPVGPPCRSRDCRC 75

RESULT 9

US-10-357-820-20
; Sequence 20, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padisaru, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Pena, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shinkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taubier, Raymond J.

;
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS

```

/ FILE REFERENCE: 21402-538B
/ CURRENT APPLICATION NUMBER: US/10/357,820
/ CURRENT FILING DATE: 2003-02-03
/ PRIOR APPLICATION NUMBER: 09/679460
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: 09/730617
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: 10/074978
/ PRIOR FILING DATE: 2002-02-12
/ PRIOR APPLICATION NUMBER: 10/138588
/ PRIOR FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: 60/387002
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: 60/355099
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: 60/375579
/ PRIOR FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: 60/393265
/ PRIOR FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: 401825
/ PRIOR FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 60/381666
/ PRIOR FILING DATE: 2002-05-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.

```

```
;
;
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-20
```

Query Match	Score	DB	Length
Best Local Similarity	28.2%;	62.5;	337;
Matches	33.9%;	Pred. No. 25;	
Conservative	19;	Mismatches	16;
Indels	19;	Gaps	3;

1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37
 152 AECPPGCGNGGFCNERRICECPDGFHGFHCEKALCTPRCWNGGLGCVTPGFCICPPG 207

RESULT 10

```

US-10-357-820-8
; Sequence 8, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Welzhien;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padigar, Muralidhara;
; APPLICANT: Patturajan, Veera;
; APPLICANT: Penna, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shinkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC POLYMER
; FILE REFERENCE: 21402-538B
; CURRENT APPLICATION NUMBER: US/10/074978
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679466
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730611
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387000
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/381666
; PRIOR FILING DATE: 2002-05-17
; Remaining Prior Application data re:
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 8
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-8

```

```

Query Match      28.2%; Score 62.5; DB 15; Length 343;
Best Local Similarity 33.9%; Pred. No. 26;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPPEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37
      |||
DB 155 ASCPGGCRNGGFCNERRICEDPDGFGHGHCALKCTPRCMNGGLCTVPGFCICPPG 210
      |||

```

RESULT 11

```

US-103-357-820-4
; Sequence 4: Application US/10357820
; Publication No. US2004029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Scatce J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Rameesh;
; APPLICANT: Li, Li;

```

```

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/381666
; PRIOR FILING DATE: 2002-05-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-6

Query Match      28.2%; Score 62.5; DB 15; Length 365;
Best Local Similarity 33.9%; Pred.No.27; Indels 19; Gaps
Matches 19; Conservative 2; Mismatches 16;

QY      1  ADGNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db      180  ACPGGCGRGFCNERRICECDGFHGHPCXALCTPCRWNGSLCVPFGCICPPG 233

RESULT 13
US-10-357-820-10
; Sequence 10, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padigar, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Pena, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shimkete, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SA
; FILE REFERENCE: 21402-538B
; CURRENT APPLICATION NUMBER: US/10/357,820
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579

```


RESULT 16
US-09-909-320-4
; Sequence 4, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-4
Query Match 28.2%; Score 62.5; DB 9; Length 379;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;
QY 1 ADCNGAC-----SPFEVPPCRGRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGFCNERRICECPDGFPHCHERKALCTPRCMNGGLCVTPGFCICPPG 235
RESULT 17
US-09-909-088B-4
; Sequence 4, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

```

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-4

Query Match      28.2%; Score 62.5; DB 9; Length 379;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps

QY      1  ADCNGAC-----SPPEVPPCRSRDC--RCVPGLGFV--GFCIHPTG 37
DB      180  AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCWGGLCVTPGFCICPPG 235

RESULT 19
US-09-902-853-4
; Sequence 4, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350

```



```
Query Match      28.2%; Score 62.5; DB 10; Length 379;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;
```

```

Db      180  AECPGGCRNGGFCNERRICEPDGFGHPHCEKALCTPRCMNGGLCVTPGFCICPPG 235
RESULT 23
US-09-903-640-4
; Sequence 4, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-640-4

Query Match      28.2%; Score 62.5; DB 10; Length 379;
Best Local Similarity 33.9%; Prod. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps

Qy      1  ADCNGAC-----SPFEVPPCERSDC--RCVPIGLGV--GFCIHPTG 37
Db      180  AECPGGCRNGGFCNERRICEPDGFGHPHCEKALCTPRCMNGGLCVTPGFCICPPG 235
RESULT 24
US-09-908-093-4
; Sequence 4, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.

```

Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 4
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien

US-09-906-742-4
Query Match 28.2%; Score 62.5; DB 10; Length 379;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;
QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGGFCNERRICECPDGFHGPCHKALCTPRCMNGGLCVTPGFCICPPG 235
Search completed: March 28, 2005, 09:15:18
Job time : 68.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:51:20 ; Search time 30 Seconds
(without alignments)
92.067 Million cell updates/sec

Title: US-09-674-496D-8

Perfect score: 222

Sequence: 1 ADONGACSPFVPPCRDRCPVIGLVGFCIHPTG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	28.4	243	2	US-08-460-309-15
2	63	28.4	243	2	US-08-125-077-15
3	63	28.4	3075	2	US-08-460-309-5
4	63	28.4	3075	2	US-08-125-077-5
5	62.5	28.2	379	4	US-09-907-794A-4
6	62.5	28.2	379	4	US-09-905-125A-4
7	62.5	28.2	379	4	US-09-902-775A-4
8	62.5	28.2	379	4	US-09-906-700-4
9	62.5	28.2	379	4	US-09-903-603A-4
10	62.5	28.2	379	4	US-09-904-320A-4
11	62.5	28.2	379	4	US-09-909-064-4
12	62.5	28.2	379	4	US-09-905-381A-4
13	62.5	28.2	379	4	US-09-906-618-4
14	62.5	28.2	379	4	US-09-205-258-441
15	59	26.6	243	2	US-08-460-309-16
16	59	26.6	243	2	US-08-125-077-16
17	57	25.7	722	4	US-09-575-081B-12
18	56	25.2	312	4	US-09-489-039A-14078
19	55.5	25.0	195	4	US-09-252-991A-17820
20	55.5	25.0	249	4	US-09-252-991A-26035
21	54.5	24.3	965	4	US-09-538-092-650
22	54	24.3	178	4	US-09-270-767-34799
23	54	24.3	178	4	US-09-270-767-50016
24	54	24.3	199	3	US-09-232-191-19
25	54	24.3	199	3	US-09-232-200-19
26	54	24.3	199	3	US-09-232-197-19
27	54	24.3	199	3	US-09-232-201-19

28	54	24.3	199	4	US-09-232-195-19	Sequence 19, Appl
29	54	24.3	354	3	US-09-232-200-55	Sequence 55, Appl
30	54	24.3	354	3	US-09-232-197-55	Sequence 55, Appl
31	54	24.3	354	3	US-09-232-201-55	Sequence 55, Appl
32	54	24.3	354	4	US-09-232-195-55	Sequence 55, Appl
33	54	24.3	1587	4	US-09-845-583A-10	Sequence 10, Appl
34	54	24.3	1587	4	US-09-561-709B-3	Sequence 3, Appl
35	53.5	24.1	40	4	US-09-471-276-1280	Sequence 1280, Ap
36	53	23.9	57	4	US-09-270-767-34071	Sequence 34071, A
37	53	23.9	57	4	US-09-270-767-49288	Sequence 49288, A
38	53	23.9	291	4	US-09-902-540-15052	Sequence 15052, A
39	53	23.9	2254	4	US-09-949-016-9270	Sequence 9270, Ap
40	52.5	23.6	135	4	US-09-252-991A-17866	Sequence 17866, A
41	52.5	23.6	545	4	US-09-252-991A-25304	Sequence 25304, A
42	52	23.4	77	3	US-08-866-545-3	Sequence 3, Appl
43	52	23.4	77	4	US-09-627-775-3	Sequence 3, Appl
44	52	23.4	170	4	US-08-828-683A-14	Sequence 14, Appl
45	52	23.4	170	4	US-09-523-323-57	Sequence 57, Appl
46	52	23.4	197	2	US-08-505-606-1	Sequence 1, Appl
47	52	23.4	197	4	US-09-000-166-1	Sequence 1, Appl
48	52	23.4	197	4	US-09-303-262-1	Sequence 1, Appl
49	52	23.4	473	4	US-09-949-016-7944	Sequence 7944, Ap
50	51.5	23.2	177	4	US-09-270-767-46544	Sequence 46544, A
51	51	23.0	170	4	US-09-252-991A-30774	Sequence 30774, A
52	51	23.0	523	4	US-09-949-016-7438	Sequence 7438, Ap
53	51	23.0	593	1	US-07-668-648-4	Sequence 4, Appl
54	51	23.0	593	2	US-08-429-998-4	Sequence 4, Appl
55	51	23.0	593	2	US-08-431-333-4	Sequence 4, Appl
56	51	23.0	593	3	US-08-991-862-17	Sequence 17, Appl
57	51	23.0	593	4	US-09-813-156-17	Sequence 17, Appl
58	51	23.0	593	4	US-09-456-886-17	Sequence 17, Appl
59	51	23.0	593	4	US-09-824-647-17	Sequence 17, Appl
60	51	23.0	593	5	US-09-824-647-17	Sequence 17, Appl
61	51	23.0	613	4	US-09-949-016-9775	Sequence 9775, Ap
62	50.5	22.7	70	4	US-09-894-882-353	Sequence 353, App
63	50.5	22.7	90	4	US-09-198-452A-597	Sequence 597, App
64	50.5	22.7	92	4	US-09-438-185A-560	Sequence 560, App
65	50.5	22.7	138	4	US-09-252-991A-20000	Sequence 20000, A
66	50.5	22.7	179	4	US-09-252-991A-30404	Sequence 30404, A
67	50.5	22.7	484	4	US-09-252-991A-19511	Sequence 19511, A
68	50.5	22.7	1073	4	US-09-949-016-9771	Sequence 9771, Ap
69	50.5	22.7	1104	2	US-08-327-832-5	Sequence 5, Appl
70	50.5	22.7	1104	2	US-08-828-584-5	Sequence 5, Appl
71	50	22.5	61	2	US-08-785-530-6	Sequence 6, Appl
72	50	22.5	61	2	US-09-123-850-6	Sequence 6, Appl
73	50	22.5	64	4	US-09-270-767-59798	Sequence 59798, A
74	50	22.5	82	4	US-09-270-767-34427	Sequence 34427, A
75	50	22.5	82	4	US-09-270-767-49644	Sequence 49644, A
76	50	22.5	200	4	US-09-270-767-44372	Sequence 44372, A
77	50	22.5	400	2	US-08-103-170-9	Sequence 9, Appl
78	50	22.5	402	1	US-08-444-734A-6	Sequence 6, Appl
79	50	22.5	402	1	US-08-087-772A-15	Sequence 15, Appl
80	50	22.5	408	1	US-07-916-901-2	Sequence 2, Appl
81	50	22.5	408	1	US-08-351-473B-3	Sequence 3, Appl
82	50	22.5	408	3	US-08-450-962-2	Sequence 2, Appl
83	50	22.5	408	3	US-08-450-962-2	Sequence 2, Appl
84	50	22.5	408	4	US-08-848-631-2	Sequence 5, Appl
85	50	22.5	408	4	US-08-848-631-5	Sequence 5, Appl
86	50	22.5	910	4	US-09-902-540-10793	Sequence 10793, A
87	49.5	22.3	57	3	US-09-130-121-1	Sequence 1, Appl
88	49.5	22.3	57	3	US-09-068-624-1	Sequence 1, Appl
89	49.5	22.3	89	4	US-09-248-796A-28045	Sequence 28045, A
90	49.5	22.3	666	3	US-09-422-869-18	Sequence 18, Appl
91	49.5	22.3	3200	2	US-08-477-451-8	Sequence 8, Appl
92	49	22.1	58	4	US-10-044-359-2	Sequence 2, Appl
93	49	22.1	61	2	US-08-785-530-1	Sequence 1, Appl
94	49	22.1	61	2	US-09-123-850-1	Sequence 1, Appl
95	49	22.1	117	4	US-09-252-991A-17204	Sequence 17204, A
96	49	22.1	135	4	US-09-252-991A-26163	Sequence 26163, A
97	49	22.1	131	4	US-09-252-991A-21561	Sequence 21561, A
98	49	22.1	210	4	US-09-252-991A-30732	Sequence 30732, A
99	49	22.1	415	3	US-09-006-353A-6	Sequence 6, Appl
100	49	22.1	415	4	US-09-573-986-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-460-309-15
; Sequence 15, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-15
Query Match 28.4%; Score 63; DB 2; Length 243;
Best Local Similarity 46.2%; Pred. No. 5.6;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY 8 SPFEVPPCRSDRCVPIGLFVGFCI 33
Db 118 SPYEDEPC--RPCNCDPVGSLSSVCI 141
RESULT 2
US-08-125-077-15
; Sequence 15, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-15
Query Match 28.4%; Score 63; DB 2; Length 243;
Best Local Similarity 46.2%; Pred. No. 5.6;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY 8 SPFEVPPCRSDRCVPIGLFVGFCI 33
Db 118 SPYEDEPC--RPCNCDPVGSLSSVCI 141

; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-125-077-15
Query Match 28.4%; Score 63; DB 2; Length 243;
Best Local Similarity 46.2%; Pred. No. 5.6;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY 8 SPFEVPPCRSDRCVPIGLFVGFCI 33
Db 118 SPYEDEPC--RPCNCDPVGSLSSVCI 141
RESULT 3
US-08-460-309-5
; Sequence 5, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; Fragments and Uses Thereof
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

```

? PRIOR APPLICATION NUMBER: US 60/143,048
? PRIOR FILING DATE: 1999-07-07
? PRIOR APPLICATION NUMBER: US 60/145,698
? PRIOR FILING DATE: 1999-07-26
? PRIOR APPLICATION NUMBER: US 60/146,222
? PRIOR FILING DATE: 1999-07-28
? PRIOR APPLICATION NUMBER: PCT/US99/20594
? PRIOR FILING DATE: 1999-09-08
? PRIOR APPLICATION NUMBER: PCT/US99/20944
? PRIOR FILING DATE: 1999-09-13
? PRIOR APPLICATION NUMBER: PCT/US99/21090
? PRIOR FILING DATE: 1999-09-15
? PRIOR APPLICATION NUMBER: PCT/US99/21547
? PRIOR FILING DATE: 1999-09-15
? PRIOR APPLICATION NUMBER: PCT/US99/23089
? PRIOR FILING DATE: 1999-10-05
? PRIOR APPLICATION NUMBER: PCT/US99/28214
? PRIOR FILING DATE: 1999-11-29
? PRIOR APPLICATION NUMBER: PCT/US99/28313
? PRIOR FILING DATE: 1999-11-30
? PRIOR APPLICATION NUMBER: PCT/US99/28564
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/28565
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/30095
? PRIOR FILING DATE: 1999-12-16
? PRIOR APPLICATION NUMBER: PCT/US99/30911
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US99/30999
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US00/00219
? PRIOR FILING DATE: 2000-01-05
? NUMBER OF SEQ ID NOS: 423
? SEQ ID NO 4
? LENGTH: 379
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-905-125A-4

```

```

Query Match      28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred.No.9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps
                                | | | | | | | | | | | | | | | | | | | |
QY    1 ADGNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCHPTG 37
Db     180 ACPGGCGRNGFCNERRICECPDGHGHCEKALTPRCMGNGLCVTPGFCICPPG 235

RESULT 7
; Sequence 4, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
```


US-09-903-603A-4
; Sequence 4, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.16182C12
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-02-22 PCT/US00/04414
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22 US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-26 US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-28 US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-903-603A-4

Query Match 28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred. No. 9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADNGAC-----SPFEVPPCRSRTC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGGFCNERRICPCDGFHGPCHCEKALCTPRCMNGGLCVTFGFCICPPG 235

RESULT 10

US-09-904-920A-4
; Sequence 4, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2000-02-22 PCT/US00/04414
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22 US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-26 US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-28 US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-4

Query Match 28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred. No. 9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADGNGAC-----SPFEVPPCESRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGFCNERRICEPDGFGHCEKALCTPRCMNGGLCVTPGFCICPPG 235

RESULT 11

US-09-909-064-4

; Sequence 4, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-064-4

Query Match 28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred. No. 9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADGNGAC-----SPFEVPPCESRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGFCNERRICEPDGFGHCEKALCTPRCMNGGLCVTPGFCICPPG 235

RESULT 12

US-09-905-381A-4

; Sequence 4, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/905,381A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048


```
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 441
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (264)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (380)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-205-258-441

Query Match      28.2%   Score 62.5; DB 4; Length 380;
Best Local Similarity 33.9%; Pred.No.9.7; Mismatches 16; Indels 19; Gaps 3;
Matches 19; Conservative 2;

Qy 1 A D C N G A C -----S P F E V P P C R S R D C --R C V P I G L F V --G F C I H P T G 37
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 A E C P G G C R N G G F C N E R R I C E P D G F H G P H C E K A L C T P R C M N G G L C V T P G F C I C P P G 235

RESULT 15
US-08-460-309-16
; Sequence 16, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
```



```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17820
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-17820

Query Match      25.0%; Score 55.5; DB 4; Length 195;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 14; Conservative 1; Mismatches 10; Indels 7; Gaps 2;

Qy 1 ADCNGA-----CGPFVPPCR-SRDCRCVPI 25
   ||| ||| ||| ||| ||| ||| ||| |||
Db 142 ASCSTATAPVACCSATPVPPCRASPSANCTPI 173

RESULT 20
US-09-252-991A-26035
; Sequence 26035, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Matc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26035
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-26035

Query Match      25.0%; Score 55.5; DB 4; Length 249;
Best Local Similarity 51.9%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 8; Indels 3; Gaps 2;

Qy 3 CNG--ACSPFVPP-CRSRDCRCVPIG 26
   ||| ||| ||| ||| ||| ||| ||| |||
Db 136 CRGRAGSPGVPPGCRADCGSPG 162

RESULT 21
US-09-538-092-650
; Sequence 650, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
```

```
; SEQ ID NO 650
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YNL023C
; US-09-538-092-650

Query Match      24.5%; Score 54.5; DB 4; Length 965;
Best Local Similarity 30.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 17; Indels 13; Gaps 2;

Qy 3 CNGACSPFVPPCRSRD-----CRC-----VPIGLFVGFCIHP 35
   ||| ||| ||| ||| ||| ||| ||| |||
Db 473 CQRKCHPGKPPCLSDSNLVCPCGTVVVPAPVRCGKLTPTCNHP 518

RESULT 22
US-09-270-767-34799
; Sequence 34799, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34799
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-34799

Query Match      24.3%; Score 54; DB 4; Length 178;
Best Local Similarity 39.4%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 15; Indels 2; Gaps 2;

Qy 1 ADCNGACSPFVPP-CRSRDCRCVPIGLFVGFC 32
   ||| ||| ||| ||| ||| ||| ||| |||
Db 142 AGAAACHPAQIPGGCIGRCHCLGIGR-PGLC 173

RESULT 23
US-09-270-767-50016
; Sequence 50016, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50016
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-50016

Query Match      24.3%; Score 54; DB 4; Length 178;
Best Local Similarity 39.4%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 15; Indels 2; Gaps 2;

Qy 1 ADCNGACSPFVPP-CRSRDCRCVPIGLFVGFC 32
   ||| ||| ||| ||| ||| ||| ||| |||
Db 142 AGAAACHPAQIPGGCIGRCHCLGIGR-PGLC 173
```

Job time : 31 secs

```
RESULT 24
US-09-232-191-19
; Sequence 19, Application US/09232191
; Patent No. 6284487
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Fatty Acid Transport Proteins
; FILE REFERENCE: WH197-21d3ME
; CURRENT APPLICATION NUMBER: US/09/232,191
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-191-19

Query Match      24.3%; Score 54; DB 3; Length 199;
Best Local Similarity 28.6%; Pred. No. 50;
Matches 16; Conservative 5; Mismatches 7; Indels 28; Gaps 3;
```

```
Qy      4 NGAC-----SPFEV-----PPCRSRDCRCVPIGL-----FVGF 31
      :|||      |||:      |||      |||:      |||:
Db      22 DGACLLMLSPFELVQFDMEAEPVRDNOGFCIPVGLGEPGLLLTKVVSQQPFVGY 77
```

```
RESULT 25
US-09-232-200-19
; Sequence 19, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21d3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-200-19

Query Match      24.3%; Score 54; DB 3; Length 199;
Best Local Similarity 28.6%; Pred. No. 50;
Matches 15; Conservative 5; Mismatches 7; Indels 28; Gaps 3;
```

```
Qy      4 NGAC-----SPFEV-----PPCRSRDCRCVPIGL-----FVGF 31
      :|||      |||:      |||      |||:      |||:
Db      22 DGACLLMLSPFELVQFDMEAEPVRDNOGFCIPVGLGEPGLLLTKVVSQQPFVGY 77
```

Search completed: March 28, 2005, 09:02:16

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:39:59 ; Search time 92 Seconds
(without alignments)
155.545 Million cell updates/sec

Title: US-09-674-496d-8

Perfect score: 222

Sequence: 1 ADNGACSPFVPCRSRDCRCVPIGLFVGFIHPG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	100.0	37	3	AY55992 Insectici
2	155	69.8	37	3	AY55991 Insectici
3	154	69.4	37	3	AY55990 Insectici
4	76	34.2	18	4	AB85936 PALB seed
5	76	34.2	18	8	ADO21580 Pea album
6	67	30.2	158	4	AAU17088 Human sig
7	67	30.2	158	7	AD93796 Human nov
8	65	29.3	250	4	ABG12917 Novel hum
9	63	28.4	1216	4	ABG09754 Novel hum
10	63	28.4	2901	4	ABG09763 Novel hum
11	63	28.4	3075	2	AAW50892 Human lam
12	62.5	28.2	337	7	ADFA4673 Human NOV
13	62.5	28.2	337	8	ADO50858 Human NOV
14	62.5	28.2	343	7	ADFA4661 Human NOV
15	62.5	28.2	343	8	ADO50846 Human NOV
16	62.5	28.2	365	7	ADFA4659 Human NOV
17	62.5	28.2	365	7	ADFA4657 Human NOV
18	62.5	28.2	365	8	ADO50844 Human NOV
19	62.5	28.2	365	8	ADO50842 Human NOV
20	62.5	28.2	373	7	ADFA4663 Human NOV
21	62.5	28.2	373	8	ADO50848 Human NOV
22	62.5	28.2	375	7	ADFA4665 Human NOV
23	62.5	28.2	375	8	ADO50850 Human NOV
24	62.5	28.2	377	3	ADC78324 Human PRO
25	62.5	28.2	377	7	ADFA4671 Human NOV

26	62.5	28.2	377	8	ADO50856 Human NOV
27	62.5	28.2	379	2	AY08065 Human EGF
28	62.5	28.2	379	2	AY13345 Amino aci
29	62.5	28.2	379	3	AY70669 Human PRO
30	62.5	28.2	379	3	AB24397 Human PRO
31	62.5	28.2	379	3	AY44822 Human mol
32	62.5	28.2	379	4	AB80213 Human PRO
33	62.5	28.2	379	4	AB31185 Amino aci
34	62.5	28.2	379	4	AAU00822 Human imm
35	62.5	28.2	379	4	AAU12325 Human PRO
36	62.5	28.2	379	4	AB53076 Human ang
37	62.5	28.2	379	6	ABU71591 Human PRO
38	62.5	28.2	379	6	ABO17769 Novel hum
39	62.5	28.2	379	6	ABU71446 Human PRO
40	62.5	28.2	379	6	ABO25156 Novel hum
41	62.5	28.2	379	6	ABU81023 Human PRO
42	62.5	28.2	379	6	ABU71892 Human sec
43	62.5	28.2	379	6	ABO01775 Novel hum
44	62.5	28.2	379	6	ABU66723 Human PRO
45	62.5	28.2	379	6	ABU55917 Human Wnt
46	62.5	28.2	379	6	ABU54348 Human sec
47	62.5	28.2	379	6	ABU67274 Novel hum
48	62.5	28.2	379	6	ABO47363 Human sec
49	62.5	28.2	379	6	ABO434071 WIF-1 pro
50	62.5	28.2	379	6	ABU59804 Novel sec
51	62.5	28.2	379	6	ABO24994 Human sec
52	62.5	28.2	379	6	ABU64500 Human sec
53	62.5	28.2	379	6	ABU72042 Novel hum
54	62.5	28.2	379	6	ABU67346 Human sec
55	62.5	28.2	379	6	ABU67143 Novel hum
56	62.5	28.2	379	6	ABO14866 Human sec
57	62.5	28.2	379	6	ABU66999 Human sec
58	62.5	28.2	379	6	ABU69623 Novel hum
59	62.5	28.2	379	6	ABU79785 Human sec
60	62.5	28.2	379	6	ABO14805 Human sec
61	62.5	28.2	379	6	ADA45827 Novel hum
62	62.5	28.2	379	6	ADA76258 Human PRO
63	62.5	28.2	379	6	ADB29209 Human sec
64	62.5	28.2	379	6	ADA18908 Human PRO
65	62.5	28.2	379	6	ADA61531 Homo sapi
66	62.5	28.2	379	6	ADB19316 Novel hum
67	62.5	28.2	379	6	ADB27857 Human PRO
68	62.5	28.2	379	6	ADA86336 Novel hum
69	62.5	28.2	379	6	ADB15900 Human PRO
70	62.5	28.2	379	6	ADA47686 Human PRO
71	62.5	28.2	379	6	ADA18065 Human sec
72	62.5	28.2	379	6	ABO32757 Human sec
73	62.5	28.2	379	6	ADA67481 Human PRO
74	62.5	28.2	379	6	ADB30488 Human PRO
75	62.5	28.2	379	6	ADA85784 Novel hum
76	62.5	28.2	379	6	ADA96996 Human PRO
77	62.5	28.2	379	6	ADA79300 Human PRO
78	62.5	28.2	379	6	ADA87439 Novel hum
79	62.5	28.2	379	6	ADB16641 Human PRO
80	62.5	28.2	379	6	ABO34817 Human PRO
81	62.5	28.2	379	6	ADA16040 Human sec
82	62.5	28.2	379	6	ADA91733 Novel hum
83	62.5	28.2	379	6	ADB14796 Human PRO
84	62.5	28.2	379	6	ADA47194 Human sec
85	62.5	28.2	379	6	ADB18757 Novel hum
86	62.5	28.2	379	6	ADA93972 Human PRO
87	62.5	28.2	379	6	ADB19868 Novel hum
88	62.5	28.2	379	6	ADB13180 Human PRO
89	62.5	28.2	379	6	ABO43302 Novel hum
90	62.5	28.2	379	6	ADA74434 Human PRO
91	62.5	28.2	379	6	ADA42185 Human sec
92	62.5	28.2	379	6	ADB24667 Human PRO
93	62.5	28.2	379	6	ADA82191 Human PRO
94	62.5	28.2	379	6	ADA75154 Human PRO
95	62.5	28.2	379	6	ADA85232 Novel hum
96	62.5	28.2	379	6	ADA84680 Novel hum
97	62.5	28.2	379	6	ABO17495 Human PRO
98	62.5	28.2	379	6	ADB29936 Human PRO

99 62.5 28.2 379 6 ADA80464 Human PRO
100 62.5 28.2 379 6 ADA75706 Human PRO

ALIGNMENTS

RESULT 1
AAV55992
ID AAV55992 standard; peptide; 37 AA.

AC AAV55992;
XX
XX 15-MAR-2000 (first entry)
XX Insecticidal peptide leguminsuline form soybean plants.
XX
XX Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;
KW pest; Sitophilus oryzae; Ephestia kuehniella; Acyrthosiphon pisum;
KW genetically modified organism.
XX Glycine max.
OS
XX WO9958695-A1.
FN
XX 18-NOV-1999.
PD
XX 07-MAY-1999; 99WO-FR001085.
XX
XX 11-MAY-1998; 98FR-00005877.
XX
XX (NASC-) INST NAT SCI APPLIQUES LYON.
PA (INRG) INST NAT RECH AGRONOMIQUE.
XX
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;
XX WPI; 2000-062304/05.
XX
XX Use of polypeptide as insecticide, especially for controlling cereal
PT grain pests.
XX
XX Example 2; Fig 7; 38pp; French.

This sequence represents the Cys-rich peptide sequence of legume plant
derived insecticidal peptide leguminsuline corresponding to that of an
entomotoxic pea protein. The invention relates to a novel insecticidal
peptide PT (AAV55992) isolated from pea plants which has homology to the
PALB peptide (AAV55991) and to the leguminsuline from soybeans. The
insecticidal peptides preferably have the amino acid sequence:
X1CYsX2CYsX3CYsX4CYsX5CYsX6CYsX7, where X1 = 2-10 amino acids; X2 = 2-5
amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
peptides can be used to protect cereal products or plants from attack by
cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
Acyrthosiphon pisum, either directly or by genetically modifying plants
(especially cereal plants) to express the peptide in their tissues or
organs

SQ Sequence 37 AA;

Query Match 100.0%; Score 222; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 2,2e-18;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADCNGACSPPEVPPCRRDCRCVPIGLFVGFCIHPTG 37
|||||
Db 1 ADCNGACSPPEVPPCRRDCRCVPIGLFVGFCIHPTG 37

RESULT 2
AAV55991
ID AAV55991 standard; peptide; 37 AA.
XX

AC AAV55991;
XX
XX 15-MAR-2000 (first entry)
XX Insecticidal peptide PALB from pea plants.
XX
XX Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;
KW pest; Sitophilus oryzae; Ephestia kuehniella; Acyrthosiphon pisum;
KW genetically modified organism.
XX Pisum sativum.
OS
XX WO9958695-A1.
FN
XX 18-NOV-1999.
PD
XX 07-MAY-1999; 99WO-FR001085.
XX
XX 11-MAY-1998; 98FR-00005877.
XX
XX (NASC-) INST NAT SCI APPLIQUES LYON.
PA (INRG) INST NAT RECH AGRONOMIQUE.
XX
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;
XX WPI; 2000-062304/05.
XX
XX Use of polypeptide as insecticide, especially for controlling cereal
PT grain pests.
XX
XX Example 2; Fig 7; 38pp; French.

This sequence represents the Cys-rich peptide sequence of legume plant
derived insecticidal peptide PALB corresponding to that of an entomotoxic
pea protein. The invention relates to a novel insecticidal peptide PT
(AAV55992) isolated from pea plants which has homology to the PALB
peptide and to the leguminsuline from soybeans (AAV55991). The insecticidal
peptides preferably have the amino acid sequence:
X1CYsX2CYsX3CYsX4CYsX5CYsX6CYsX7, where X1 = 2-10 amino acids; X2 = 2-5
amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
peptides can be used to protect cereal products or plants from attack by
cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
Acyrthosiphon pisum, either directly or by genetically modifying plants
(especially cereal plants) to express the peptide in their tissues or
organs

SQ Sequence 37 AA;

Query Match 69.8%; Score 155; DB 3; Length 37;
Best Local Similarity 62.2%; Pred. No. 1.1e-10;
Matches 23; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ADCNGACSPPEVPPCRRDCRCVPIGLFVGFCIHPTG 37
|||||
Db 1 ASCNGVCSPPFEMPCCGTSACRCIPVGLVVGVCYCRNPSG 37

RESULT 3
AAV55990
ID AAV55990 standard; peptide; 37 AA.
XX

AC AAV55990;
XX
XX 15-MAR-2000 (first entry)
XX Insecticidal peptide PT from pea plants.
XX
XX Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;
KW pest; Sitophilus oryzae; Ephestia kuehniella; Acyrthosiphon pisum;
KW genetically modified organism.
XX Pisum sativum.
OS

```
XX WO9958695-A1.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-FR001085.
PF
XX
XX 11-MAY-1998; 98FR-00005877.
PR
XX
XX (NASC-) INST NAT SCI APPLIQUES LYON.
PA
XX (INRG) INST NAT RECH AGRONOMIQUE.
PA
XX
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;
PI
XX WPI; 2000-062304/05.
XX
XX Use of polypeptide as insecticide, especially for controlling cereal
PT
XX grain pests.
PT
XX
XX Example 2; Fig 7; 38pp; French.
PS
XX
XX This sequence represents the Cys-rich peptide sequence of legume plant
CC
XX derived insecticidal peptide PT corresponding to that of an entomotoxic
CC
XX pea protein. The peptide has homology to the known insecticidal peptides
CC
XX Palb (AAV55991) from peas or legumins (AAV55992) from soybeans. The
CC
XX insecticidal peptides preferably have the amino acid sequence:
CC
XX XI1Cys2Cys3Cys4Cys5Cys6Cys7 where X1 = 2-10 amino acids; X2 = 2-5
CC
XX amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
CC
XX acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
CC
XX peptide can be used to protect cereal products or plants from attack by
CC
XX cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
CC
XX Acyrthosiphon pisum, either directly or by genetically modifying plants
CC
XX (especially cereal plants) to express the peptide in their tissues or
CC
XX organs
XX
XX Sequence 37 AA;
SQ
Query Match 69.4%; Score 154; DB 3; Length 37;
Best Local Similarity 59.5%; Pred. No. 1.5e-10;
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPPCRSDRCRCVPIGLFVGFCIHPTG 37
DB 1 ASCNGVCSPEMPPCGTSACRCIPVGLVIGYCRNPSG 37
RESULT 4
AAB85936
ID AAB85936 standard; peptide; 18 AA.
XX
XX AAB85936;
AC
XX
XX 30-NOV-2001 (first entry)
DT
XX
XX Palb seed storage protein fragment.
DE
XX
XX Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
KW
XX 2A11; PA1B.
KW
XX
XX Unidentified.
OS
XX
XX US6281410-B1.
PN
XX
XX 28-AUG-2001.
PD
XX
XX 15-JAN-1999; 99US-00232861.
PF
XX
XX 31-JUL-1986; 86US-00891529.
PR
XX 26-MAY-1987; 87US-00054369.
PR
XX 28-JUL-1987; 87US-00078538.
PR
XX 25-JAN-1988; 88US-00147781.
PR
XX 15-MAR-1988; 88US-00168190.
PR
XX 29-APR-1988; 88US-00188361.
PR
02-NOV-1988; 88US-00267685.
PR
21-MAY-1990; 90US-00526123.
PR
09-JUL-1990; 90US-00550804.
PR
10-AUG-1993; 93US-00105852.
PR
07-JUN-1995; 95US-00484941.
PR
07-MAR-1997; 97US-00812665.
PR
XX
XX (CALJ) CALGENE LLC.
PA
XX
XX Knauf VC, Kridl JC;
XX
XX WPI; 2001-564354/63.
XX
XX Obtaining a plant that produces a seed with a modified phenotype or
PT
XX altering a seed phenotype, comprises transforming a plant cell with a DNA
PT
XX construct consisting of operably linked components in the direction of
PT
XX transcription.
XX
XX Example 9; Fig 6; 68pp; English.
PS
XX
XX The invention provides a method for obtaining a plant which produces at
CC
XX least one seed having a modified phenotype. The method involves
CC
XX transforming a host plant cell with a DNA construct which consists of
CC
XX operably linked components in the direction of transcription, a promoter
CC
XX region from a Brassica plant gene, a DNA sequence of interest other than
CC
XX the native coding sequence, and a transcription termination region. The
CC
XX method is useful for obtaining plants having modified phenotype or for
CC
XX altering the phenotype of a plant seed or tissue. The DNA constructs are
CC
XX used in manipulating plant cells to provide for regulated transcription,
CC
XX such as light inducible transcription, in a plant tissue or plant part of
CC
XX interest at particular stages of plant growth or in response to external
CC
XX control. These constructs are also used for modulation of expression of
CC
XX endogenous products as well as production of exogenous products in the
CC
XX seed. Sequences AAB85936-39 represent fragments of storage proteins used
CC
XX in comparison studies with the storage protein 2A11
XX
XX Sequence 18 AA;
SQ
Query Match 34.2%; Score 76; DB 4; Length 18;
Best Local Similarity 64.7%; Pred. No. 0.073;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 7 CSPFEVPPCRSDRCRCV 23
DB 2 CSPFDIPPGSLCRCI 18
RESULT 5
ADO21580
ID ADO21580 standard; peptide; 18 AA.
XX
XX ADO21580;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Pea albumin 1b reactive site.
DE
XX
XX Pea; fruit specific promoter; plant; transgenic; protein storage;
KW
XX improved nutrient source; enhanced response to light;
KW
XX dehydration resistance; herbicide resistance; pest resistance; 2A11 gene;
KW
XX protease inhibitor.
XX
XX Pisum sativum.
OS
XX
XX US2004055038-A1.
PN
XX
XX 18-MAR-2004.
PD
XX
XX 12-FEB-2001; 2001US-00782130.
XX
XX 17-JAN-1985; 85US-00692605.
PR
XX 31-JUL-1986; 86US-00891529.
PR
XX 26-MAY-1987; 87US-00054369.
PR
```

PR 28-JUL-1987; 87US-00078538.
 PR 25-JAN-1988; 88US-00147781.
 PR 15-MAR-1988; 88US-00168190.
 PR 29-APR-1988; 88US-00188361.
 PR 02-NOV-1988; 88US-00367685.
 PR 21-MAY-1990; 90US-00526123.
 PR 09-JUL-1990; 90US-00550804.
 PR 14-SEP-1990; 90US-00582241.
 PR 08-AUG-1991; 91US-00742834.
 PR 10-AUG-1993; 93US-00105852.
 PR 07-JUN-1995; 95US-00484941.
 PR 07-MAR-1997; 97US-00812665.
 PR 15-JAN-1999; 99US-00232861.
 XX
 PA (KNAU/) KNAUF V C.
 PA (KRIDL/) KRIDL J C.
 XX
 PI Knauf VC, Kridl JC;
 XX
 DR WPI; 2004-247819/23.
 XX
 PT New DNA construct comprising a promoter region, a DNA sequence of
 PT interest and a transcription termination region, useful for producing
 PT transgenic plants.
 XX
 ES Example 9; Fig 6; 69pp; English.
 CC
 CC The invention relates to a DNA construct comprising, as operably linked
 CC components in the direction of transcription, a promoter region
 CC obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier
 CC protein (ACP) gene, a DNA sequence of interest other than the native
 CC coding sequence of the gene and a transcription termination region, where
 CC the components are functional in a plant cell and where the DNA construct
 CC is flanked by T-DNA. Also included are a plant cell having an altered
 CC phenotype as a result of expression of a DNA construct, a plant
 CC comprising cells comprising a DNA construct, a seed obtained from the
 CC plant, obtaining a plant having a modified phenotype or modifying the
 CC genotype of a plant to impart a desired characteristic to seed as
 CC distinct from other plant tissue, altering the phenotype of plant seed
 CC tissue or modifying transcription in seed tissue as distinct from other
 CC plant tissue and selectively expressing a heterologous DNA sequence of
 CC interest in seed tissue as distinct from other plant tissue. The DNA
 CC construct is useful in modifying or altering the genotype or phenotype of
 CC a plant to impart a desired characteristic. The construct is also useful
 CC in regulating genetic modification of plant or regulating tissue and/or
 CC developmental specific transcription and expression in plants. The plants
 CC produced have increased capability of protein storage, improved nutrient
 CC source, enhanced response to light and dehydration resistance and
 CC resistant to herbicide and pests. The seed specific promoters are from
 CC the Napin, ACP and EA9 genes and the fruit specific promoter is from the
 CC tomato 2A11 gene. The present sequence is a reactive site from a protein
 CC similar to the tomato 2A11 protein (thought to be a protease inhibitor).
 XX
 SQ Sequence 18 AA;
 Query Match 34.2%; Score 76; DB 8; Length 18;
 Best Local Similarity 64.7%; Freq. No. 0.073;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CSPFVPPPCRSRCRCV 23
 Db 2 CSPFDIPPGCSPLCRCI 18
 ||||:|||||
 RESULT 6
 AAU17088
 ID AAU17088 standard; protein; 158 AA.
 XX
 AC AAU17088;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Novel signal transduction pathway protein, Seq ID 653.

XX
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KW reproductive system; gastrointestinal; liver disorder; AIDS;
 KW acquired immune deficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200154733-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001312.
 XX
 PF 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 18-AUG-2000; 2000US-0225759P.
 PR 22-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0228668P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 06-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.

```
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234233P.
PR 21-SEP-2000; 2000US-0234234P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0244647P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Roen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX N-PSDB; AAS27005.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cancers, immune
XX disorders and neuronal disorders.
XX
XX Claim 1; SEQ ID NO 653; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
XX diagnosing, preventing and treating diseases including immune system
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
XX transplant rejections and graft versus host disease, infectious diseases
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
XX other blood-related disorders (sickle cell anaemia), myeloproliferative
XX disorders, primary haematopoietic disorders, hyperproliferative disorders
XX (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
XX Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
XX (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
XX glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
XX respiratory disorders, dermatological disorders, in wound healing,
XX epithelial cell proliferation, endocrine disorders (e.g. Addison's
XX disease), reproductive system disorders, gastrointestinal disorder
XX (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
XX B-cell responsiveness to pathogens, activators of T-cells, to induce
XX higher affinity antibodies, and as a means to induce tumour proliferation
XX in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU1059-
XX AAU17683 represent novel signal transduction pathway protein, amino acid
XX sequences of the invention
XX
XX
XX Query Match 30.2%; Score 67; DB 4; Length 158;
XX Best Local Similarity 32.6%; Pred. No. 5.4;
XX Matches 14; Conservative 5; Mismatches 14; Indels 10; Gaps 1;
XX
XX Qy 5 GACSPFEVPCRSRDCRCVPIGLFVGFC-----IHPTG 37
XX Db 96 GGQPSQPPPARASQCQPQSLQLFLGFCSQLVGPPTCALHPRG 138
XX
XX
XX RESULT 7
XX ADB93796
XX ID ADB93796 standard; protein; 158 AA.
XX
XX AC ADB93796;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE Human novel protein #30.
XX
XX human; autoimmune disease; Parkinson's disease; silicosis;
XX gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
XX immunosuppressive agent; adjuvant; enhance immune response;
XX higher affinity antibody induction;
XX increased serum immunoglobulin concentration.
XX
```


XX	WPI; 1998-240534/21.
XX	
XX	Use of laminin and fragments - for developing products for use in the
PT	diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
FT	CUD.
XX	
XX	Claim 15; Page 80-85; 132pp; English.
XX	
CC	This is the amino acid sequence of the human laminin A chain. The primary
CC	object of the invention is to use laminin, laminin-derived protein
CC	fragments and/or laminin-derived polypeptides as potent inhibitors of
CC	amyloid formation, deposition, accumulation and/or persistence in
CC	Alzheimer's disease and other amyloidoses. The laminin products (see
CC	AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1
CC	or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular
CC	repeats of the laminin A1 chain and the beta-amyloid binding domain of
CC	the laminin A chain. A claimed method for treating an amyloid disease
CC	comprises administering a polypeptide having a conformational similarity
CC	to a fragment of a laminin protein. A method for diagnosing an amyloid
CC	disease involves determining levels of laminin in a sample. Production of
CC	laminin or its fourth globular repeat in vivo provides a method for in
CC	vivo inhibition of beta-amyloid amyloidoses. The products and methods can
CC	be used for the diagnosis, prognosis, monitoring and treatment of
CC	amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary
CC	cerebral haemorrhage with amyloidosis of the Dutch type (where the
CC	specific amyloid is the beta-amyloid protein), the amyloidosis associated
CC	with chronic inflammation, various forms of malignancy and Familial
CC	Mediterranean Fever (AA amyloid or inflammation-association amyloidosis),
CC	the amyloidosis associated with multiple myeloma and other B-cell
CC	abnormalities (AL amyloid), the amyloidosis associated with type II
CC	diabetes (anlylin or islet amyloid), the amyloidosis associated with prion
CC	diseases including Creutzfeldt-Jacob disease, Gerstmann-Straussler
CC	syndrome, kuru and animal scrapie (prp amyloid), the amyloidosis
CC	associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC	2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC	amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or
CC	transthyretin amyloid), and the amyloidosis associated with endocrine
CC	tumours such as medullary carcinoma of the thyroid (variant of
CC	procalcitonin)
XX	
SQ	Sequence 3075 AA;
	Query Match 28.4%; Score 63; DB 2; Length 3075;
	Best Local Similarity 46.2%; Pred. No. 2-2e+02;
	Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY	8 SPEVPPCNRDRCRVPGLGVGFCCI 33 : : :
Db	387 SPYEDEPC--RPCNCDFVGSLSVCI 410
RESULT 12	
ID	ADF44673 standard; protein; 337 AA.
XX	
AD	ADF44673;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Human NOV1j protein SEQ ID NO:20.
XX	
KW	human; antidiabetic; anorectic; cardiant; hypotensive;
KW	antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW	protozoacide; antihelmintic; nootropic; neuroprotective;
KW	antiparkinsonian; anticoagulant; osteopathic; antiarthritic;
KW	antiinflammatory; dermatological; antiasthmatic; antilipaemic; vulnery;
KW	antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;
KW	infectious disease; anorexia; cancer; cardiovascular disease;
KW	hypertension; atherosclerosis; neurodegenerative disorder;
KW	Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW	osteoarthritis; haematopoietic disorder; inflammatory skin disorder;
KW	asthma; dyslipidaemia.

```
XX OS Homo sapiens.
XX PN WO2003066881-A2.
XX PD 14-AUG-2003.
XX PF 03-FEB-2003; 2003WO-US003403.
XX PR 08-FEB-2002; 2002US-0355099P.
XX PR 12-FEB-2002; 2002US-00074978.
XX PR 12-FEB-2002; 2002US-0356424P.
XX PR 19-FEB-2002; 2002US-0357928P.
XX PR 21-FEB-2002; 2002US-0358608P.
XX PR 27-FEB-2002; 2002US-0359860P.
XX PR 25-APR-2002; 2002US-0375579P.
XX PR 01-MAY-2002; 2002US-00138588.
XX PR 17-MAY-2002; 2002US-0381666P.
XX PR 07-JUN-2002; 2002US-0387002P.
XX PR 02-JUL-2002; 2002US-0393285P.
XX PR 07-AUG-2002; 2002US-0401825P.
XX PA (CURA-) CURAGEN CORP.
XX PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;
PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;
PI Stone DJ, Taupier RJ;
XX OS Homo sapiens.
XX PN WPI; 2003-748127/70.
XX PR N-PSDB; ADF44672.
XX PT New isolated NOVX polypeptides and polynucleotides, useful for
XX PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
XX PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
XX PT asthma, or infections.
XX PS Claim 1; SEQ ID NO 20; 234pp; English.
XX CC The present invention describes an isolated polypeptide (I) comprising:
XX CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n
XX CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a
XX CC sequence that is at least 95% identical to (P), or having one or more
XX CC conservative amino acid substitutions in. (I) can be encoded by a nucleic
XX CC acid molecule (II), where the sequence is selected from the group
XX CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,
XX CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
XX CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,
XX CC neotropic, neuroprotective, antiparkinsonian, anticonvulsant,
XX CC osteopathic, antiarthritic, antiinflammatory, dermatological,
XX CC antiasthmatic, antilipemic, vulnerary and antiangiogenic activities, and
XX CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules
XX CC (II) and antibodies that immunospecifically bind (I), can be used in the
XX CC manufacture of a medicament for treating a syndrome associated with a
XX CC human disease. They are useful for treating, preventing or diagnosing
XX CC diseases such metabolic disorders, diabetes, obesity, infectious diseases
XX CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,
XX CC cardiovascular diseases (hypertension, atherosclerosis),
XX CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,
XX CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,
XX CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and
XX CC (II) may also be used as targets for the identification of small
XX CC molecules that modulate or inhibit e.g. neurogenesis, cell
XX CC differentiation, cell proliferation, haematopoiesis, wound healing and
XX CC angiogenesis, in gene therapy, in gene ration of antibodies that bind
XX CC immunospecifically to (I) for use in therapeutic or diagnostic methods.
XX CC (I) can also be used as hybridisation probes, in chromosome mapping,
XX CC tissue typing, preventive medicine, and pharmacogenomics. The present
XX CC sequence is used in the exemplification of the present invention.
XX SQ Sequence 337 AA;
Query Match 28.2%; Score 62.5; DB 7; Length 337;
Best Local Similarity 33.9%; Pred. No. 35;
```

```
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;
Qy 1 ADCNGAC-----SPFEVPPCRSRTC--RCVPIGLFV--GFCIHPTG 37
Db 152 AECPGGCRNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPG 207
RESULT 13
ADO50858
ID ADO50858 standard; protein; 337 AA.
XX AC ADO50858;
XX DT 15-JUL-2004 (first entry)
XX DE Human NOV1j protein.
XX KW NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;
XX KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;
XX KW infection; haemophilia; graft-versus-host disease; AIDS;
XX KW acquired immune deficiency syndrome; asthma; Crohn's disease;
XX KW multiple sclerosis; anorexia; cancer-associated cachexia;
XX KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX KW haematopoietic disorder; dyslipidaemia; wasting disorder;
XX KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
XX KW gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN US2004029140-A1.
XX PD 12-FEB-2004.
XX PF 16-JUL-2003; 2003US-00357820.
XX PR 04-OCT-2000; 2000US-00679460.
XX PR 05-DEC-2000; 2000US-00730617.
XX PR 08-FEB-2002; 2002US-0355099P.
XX PR 12-FEB-2002; 2002US-00074978.
XX PR 19-FEB-2002; 2002US-0357928P.
XX PR 21-FEB-2002; 2002US-0358608P.
XX PR 27-FEB-2002; 2002US-0359860P.
XX PR 25-APR-2002; 2002US-0375579P.
XX PR 01-MAY-2002; 2002US-00138588.
XX PR 17-MAY-2002; 2002US-0381666P.
XX PR 07-JUN-2002; 2002US-0387002P.
XX PR 02-JUL-2002; 2002US-0393265P.
XX (ANDE/) ANDERSON D W.
XX PA (BURG/) BURGESS C E.
XX PA (CASM/) CASMAN S J.
XX PA (GORM/) GORMAN L.
XX PA (JIWV/) JI W.
XX PA (KEKU/) KEKUDA R.
XX PA (LILL/) LI L.
XX PA (PADI/) PADIGARU M.
XX PA (PATT/) PATTURAJAN M.
XX PA (PENP/) PENNA C E A.
XX PA (SHEN/) SHENOY S G.
XX PA (SHIM/) SHIMKETS R A.
XX PA (STON/) STONE D J.
XX PA (TAUP/) TAUPIER R J.
XX PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;
XX PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;
XX PI Stone DJ, Taupier RJ;
XX WPI; 2004-179665/17.
XX DR N-PSDB; ADO50857.
XX PT New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,
XX PT atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and
XX PT in chromosome mapping, tissue typing or pharmacogenomics.
```

XX PS Claim 1; SEQ ID NO 20; 119pp; English.

XX CC The present invention relates to novel NOVX polypeptides and their

CC encoding polynucleotides. The invention is useful in diagnosing, treating

CC and preventing NOVX-associated disorders such as cardiomyopathy,

CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune

CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,

CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as

CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,

CC dyslipidaemias and other wasting disorders associated with chronic

CC diseases. The invention is also useful as hybridisation probes, in

CC chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. The invention is also useful in gene therapy and in the

CC preparation of vaccines. The present sequence is human NOVX protein.

XX SQ Sequence 337 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 337;

Best Local Similarity 33.9%; Pred. No. 35;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37

Db 152 AECFGGCRNGGFCNERRICECPDGFHGHCEKALCTPRCWNGLCVTPGFCICPPG 207

RESULT 14

ADF44661

ID ADF44661 standard; protein; 343 AA.

AC ADF44661;

XX 12-FEB-2004 (first entry)

DT Human NOV1d protein SEQ ID NO:8.

DE human; antidiabetic; anorectic; cardiant; hypotensive;

XX antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;

KW protozoacide; antihelminthic; nootropic; neuroprotective;

KW antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;

KW antiinflammatory; dermatological; antiasthmatic; antipneumonic;

KW antiangiogenic; gene therapy; metabolic disorder; diabetes; vulnary;

KW infectious disease; anorexia; cancer; cardiovascular disease;

KW hypertension; atherosclerosis; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;

KW osteoarthritis; haematopoietic disorder; inflammatory skin disorder;

KW asthma; dyslipidaemia.

XX Homo sapiens.

XX W02003066881-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-US003403.

XX 08-FEB-2002; 2002US-0355099P.

PR 12-FEB-2002; 2002US-00074978.

PR 12-FEB-2002; 2002US-0356424P.

PR 13-FEB-2002; 2002US-0357928P.

PR 21-FEB-2002; 2002US-0358608P.

PR 27-FEB-2002; 2002US-0359860P.

PR 25-APR-2002; 2002US-0375579P.

PR 01-MAY-2002; 2002US-00138588.

PR 17-MAY-2002; 2002US-0381666P.

PR 07-JUN-2002; 2002US-0387002P.

PR 02-JUL-2002; 2002US-0393265P.

PR 07-AUG-2002; 2002US-0401825P.

XX (CURA-) CURAGEN CORP.

PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shinkets RA;

PI Stone DJ, Taupier RJ;

XX WPI; 2003-748127/70.

DR N-PSDB; ADF44660.

XX New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX Claim 1; SEQ ID NO 8; 234pp; English.

XX The present invention describes an isolated polypeptide (I) comprising:

CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n

CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a

CC sequence that is at least 95% identical to (P), or having one or more

CC conservative amino acid substitutions in. (I) can be encoded by a nucleic

CC acid molecule (II), where the sequence is selected from the group

CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,

CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,

CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,

CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,

CC osteopathic, antiarthritic, antiinflammatory, dermatological,

CC antiasthmatic, antipneumonic, vulnary and antiangiogenic activities, and

CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules

CC (II) and antibodies that immunospecifically bind (I), can be used in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease. They are useful for treating, preventing or diagnosing

CC diseases such as metabolic disorders, diabetes, obesity, infectious diseases

CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,

CC cardiovascular diseases (hypertension, atherosclerosis),

CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,

CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,

CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and

CC (II) may also be used as targets for the identification of small

CC molecules that modulate or inhibit e.g. neurogenesis, cell

CC differentiation, cell proliferation, haematopoiesis, wound healing and

CC angiogenesis, in gene therapy, in gene ration of antibodies that bind

CC immunospecifically to (I) for use in therapeutic or diagnostic methods.

CC (I) can also be used as hybridisation probes, in chromosome mapping,

CC tissue typing, preventive medicine, and pharmacogenomics. The present

CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 343 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 343;

Best Local Similarity 33.9%; Pred. No. 36;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37

Db 155 AECFGGCRNGGFCNERRICECPDGFHGHCEKALCTPRCWNGLCVTPGFCICPPG 210

RESULT 15

ADO50846

ID ADO50846 standard; protein; 343 AA.

XX ADO50846;

AC ADO50846;

DT 15-JUL-2004 (first entry)

XX Human NOV1d protein.

XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

KW infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;

KW multiple sclerosis; anorexia; cancer-associated cachexia;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW haematopoietic disorder; dyslipidaemia; wasting disorder;

KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
 KW gene therapy; vaccine; human.

OS Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

XX (BURG/) BURGESS C E.

XX (CASM/) CASMAN S J.

XX (GORM/) GORMAN L.

XX (JIW/) JI W.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (PADI/) PADIGARU M.

XX (PATT/) PATTURAJAN M.

XX (PENA/) PENNA C E A.

XX (SHEN/) SHENOY S G.

XX (SHIM/) SHIMKETS R A.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX WPI; 2004-179665/17.

XX N-PSDB; ADO50845.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

XX atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and

XX in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; SEQ ID NO 8; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their

XX encoding polynucleotides. The invention is useful in diagnosing, treating

XX and preventing NOVX-associated disorders such as cardiomyopathy,

XX atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

XX infections, haemophilia, graft-versus-host disease, AIDS (acquired immune

XX deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,

XX anorexia, cancer-associated cachexia, neurodegenerative disorders such as

XX Alzheimer's disease, Parkinson's disease, haematopoietic disorders,

XX dyslipidaemias and other wasting disorders associated with chronic

XX diseases. The invention is also useful as hybridisation probes, in

XX chromosome mapping, tissue typing, preventive medicine and

XX pharmacogenomics. The invention is also useful in gene therapy and in the

XX preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 343 AA;

XX Query Match 28.2%; Score 62.5; DB 8; Length 343;

XX Best Local Similarity 33.9%; Pred. No. 36;

XX Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

XX 1 ADCNGAC-----SPFEVPPCRSDDC--RCVPIGLFV--GFCIHPTG 37

Db RESULT 16
 ADF44659
 ID ADF44659 standard; protein; 365 AA.
 XX ADF44659;
 AC ADF44659;
 XX 12-FEB-2004 (first entry)
 DT Human NOV1c protein SEQ ID NO:6.
 XX human; antidiabetic; anorectic; cardiant; hypotensive;
 KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
 KW protozoacide; antihelminthic; nootropic; neuroprotective;
 KW antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;
 KW antiinflammatory; dermatological; antiasthmatic; antilipaemic; vulnary;
 KW antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;
 KW infectious disease; anorexia; cancer; cardiovascular disease;
 KW hypertension; atherosclerosis; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
 KW osteoarthritis; haematopoietic disorder; inflammatory skin disorder;
 KW asthma; dyslipidaemia.
 KW Homo sapiens.
 OS OS
 XX WO2003066881-A2.
 XX 14-AUG-2003.
 PD 03-FEB-2003; 2003WO-US003403.
 XX 08-FEB-2002; 2002US-0355099P.
 XX 12-FEB-2002; 2002US-00074978.
 PR 12-FEB-2002; 2002US-0356424P.
 PR 19-FEB-2002; 2002US-0357928P.
 PR 21-FEB-2002; 2002US-0358608P.
 PR 27-FEB-2002; 2002US-0359860P.
 PR 25-APR-2002; 2002US-0375579P.
 PR 01-MAY-2002; 2002US-00138588.
 PR 17-MAY-2002; 2002US-0381666P.
 PR 07-JUN-2002; 2002US-0387002P.
 PR 02-JUL-2002; 2002US-0393265P.
 PR 07-AUG-2002; 2002US-0401825P.
 XX (CURA-) CURAGEN CORP.
 PA Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;
 PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;
 PI Stone DJ, Taupier RJ;
 PI WPI; 2003-748127/70.
 DR N-PSDB; ADF44659.
 DR New isolated NOVX polypeptides and polynucleotides, useful for
 XX preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.
 XX Claim 1; SEQ ID NO 6; 234pp; English.
 PS The present invention describes an isolated polypeptide (I) comprising:
 XX (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n
 CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a
 CC sequence that is at least 95% identical to (P), or having one or more
 CC conservative amino acid substitutions in. (I) can be encoded by a nucleic
 CC acid molecule (II), where the sequence is selected from the group
 CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,
 CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
 CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,
 CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,

NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;
 KW multiple sclerosis; anorexia; cancer-associated cachexia;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW haematopoietic disorder; dyslipidaemia; wasting disorder;
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
 KW gene therapy; vaccine; human.

XX Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

XX (BURG/) BURGESS C E.

XX (CASM/) CASMAN S J.

XX (GORM/) GORMAN L.

XX (JIWW/) JI W.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (PADI/) PADIGARU M.

XX (PATT/) PATTURAJAN M.

XX (PENA/) PENA C E A.

XX (SHEN/) SHENOY S G.

XX (SHIM/) SHIMKETS R A.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

XX Li L, Padigar M, Patturajan M, Pena CE, Shenoy SG, Shimkets RA;

XX Stone DJ, Taupier RJ;

XX WPI; 2004-179665/17.

XX N-PSDB; ADO50843.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

XX atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and

XX in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; SEQ ID NO 6; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their

XX encoding polynucleotides. The invention is useful in diagnosing, treating

XX and preventing NOVX-associated disorders such as cardiomyopathy,

XX atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

XX infections, haemophilia, graft-versus-host disease, AIDS (acquired immune

XX deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,

XX anorexia, cancer-associated cachexia, neurodegenerative disorders such as

XX Alzheimer's disease, Parkinson's disease, haematopoietic disorders,

XX dyslipidaemias and other wasting disorders associated with chronic

XX diseases. The invention is also useful as hybridisation probes, in

XX chromosome mapping, tissue typing, preventive medicine and

XX pharmacogenomics. The invention is also useful in gene therapy and in the

XX preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 365 AA;

XX Query Match

XX 28.2%; Score 62.5; DB 8; Length 365;

RESULT 19

ADO50842

ID ADO50842 standard; protein; 365 AA.

XX AC ADO50842;

XX 15-JUL-2004 (first entry)

XX Human NOV1b protein.

XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

XX atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

XX infection; haemophilia; graft-versus-host disease; AIDS;

XX acquired immune deficiency syndrome; asthma; Crohn's disease;

XX multiple sclerosis; anorexia; cancer-associated cachexia;

XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

XX haematopoietic disorder; dyslipidaemia; wasting disorder;

XX chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;

XX gene therapy; vaccine; human.

XX OS Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

XX (BURG/) BURGESS C E.

XX (CASM/) CASMAN S J.

XX (GORM/) GORMAN L.

XX (JIWW/) JI W.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (PADI/) PADIGARU M.

XX (PATT/) PATTURAJAN M.

XX (PENA/) PENA C E A.

XX (SHEN/) SHENOY S G.

XX (SHIM/) SHIMKETS R A.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

XX Li L, Padigar M, Patturajan M, Pena CE, Shenoy SG, Shimkets RA;

XX Stone DJ, Taupier RJ;

XX WPI; 2004-179665/17.

XX N-PSDB; ADO50841.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

XX atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and

XX in chromosome mapping, tissue typing or pharmacogenomics.

PT in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; SEQ ID NO 4; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their
XX encoding polynucleotides. The invention is useful in diagnosing, treating
XX and preventing NOVX-associated disorders such as cardiomyopathy,
XX atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
XX deficiencies, haemophilia, graft-versus-host disease, AIDS (acquired immune
XX deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,
XX anorexia, cancer-associated cachexia, neurodegenerative disorders such as
XX Alzheimer's disease, Parkinson's disease, haematopoietic disorders,
XX dyslipidaemias and other wasting disorders associated with chronic
XX diseases. The invention is also useful as hybridisation probes, in
XX chromosome mapping, tissue typing, preventive medicine and
XX pharmacogenomics. The invention is also useful in gene therapy and in the
XX preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 365 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 365;

Best Local Similarity 33.9%; Pred. No. 38;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCKSRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPG 235

RESULT 20

ADF4663

ID ADF4663 standard; protein; 373 AA.

XX ADF4663;

DT 12-FEB-2004 (first entry)

DE Human NOV1e protein SEQ ID NO:10.

XX human; antidiabetic; anorectic; cardiant; hypotensive;
XX antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
XX protozoacide; antihelminthic; nootropic; neuroprotective;
XX antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;
XX antiinflammatory; dermatological; antiasthmatic; antilipaeamic;
XX antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;
XX infectious disease; anorexia; cancer; cardiovascular disease;
XX hypertension; atherosclerosis; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
XX osteoarthritis; haematopoietic disorder; inflammatory skin disorder;
XX asthma; dyslipidaemia.

XX Homo sapiens.

XX WO2003066881-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-US003403.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 12-FEB-2002; 2002US-0356424P.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358080P.

XX 27-FEB-2002; 2002US-0375579P.

XX 25-APR-2002; 2002US-00138588.

XX 01-MAY-2002; 2002US-0381666P.

XX 17-MAY-2002; 2002US-0387002P.

XX 07-JUN-2002; 2002US-0393265P.

XX 02-JUL-2002; 2002US-0393265P.

XX 07-AUG-2002; 2002US-0401825P.

XX (CURA-) CURAGEN CORP.

XX

PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

PI Li L, Padigaru M, Patturajan M, Pena CE, Shenoy SG, Shinkets RA;

PI Stone DJ, Taupier RJ;

XX

DR WPI; 2003-748127/70.

DR N-PSDB; ADF44662.

XX

XX New isolated NOVX polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOVX-associated disorders, e.g.
XX osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
XX asthma, or infections.

PS Claim 1; SEQ ID NO 10; 234pp; English.

CC The present invention describes an isolated polypeptide (I) comprising:

CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n
CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a
CC sequence that is at least 95% identical to (P), or having one or more
CC conservative amino acid substitutions in. (I) can be encoded by a nucleic
CC acid molecule (II), where the sequence is selected from the group
CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,

CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,
CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,
CC osteopathic, antiarthritic, antilipaeamic, antiinflammatory, dermatological,
CC antiasthmatic, antiparkinsonian, antiparkinsonian, anticonvulsant,
CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules
CC (II) and antibodies that immunospecifically bind (I), can be used in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease. They are useful for treating, preventing or diagnosing
CC diseases such as metabolic disorders, diabetes, obesity, infectious diseases
CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,
CC cardiovascular diseases (hypertension, atherosclerosis),
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,
CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and
CC (II) may also be used as targets for the identification of small
CC molecules that modulate or inhibit e.g. neurogenesis, cell
CC differentiation, cell proliferation, haematopoiesis, wound healing and
CC angiogenesis, in gene therapy, in gene ration of antibodies that bind
CC immunospecifically to (I) for use in therapeutic or diagnostic methods.

CC (I) can also be used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 373 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 373;

Best Local Similarity 33.9%; Pred. No. 39;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCKSRDC--RCVPIGLFV--GFCIHPTG 37

Db 185 AECPGGCRNGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPG 240

RESULT 21

AD050848

ID AD050848 standard; protein; 373 AA.

XX AD050848;

DT 15-JUL-2004 (first entry)

DE Human NOV1e protein.

XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

XX atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

XX infection; haemophilia; graft-versus-host disease; AIDS;

XX acquired immune deficiency syndrome; asthma; Crohn's disease;

XX multiple sclerosis; anorexia; cancer-associated cachexia;

XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW haematopoietic disorder; dyslipidaemia; wasting disorder;
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
 KW gene therapy; vaccine; human.

XX Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 03-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 23-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

PA (BURG/) BURGESS C E.

PA (CASM/) CASMAN S J.

PA (GORM/) GORMAN L.

PA (JIW/) JI W.

PA (KEKU/) KEKUDA R.

PA (LILL/) LI L.

PA (PADI/) PADIGARU M.

PA (PATT/) PATTURAJAN M.

PA (PENA/) PENA C E A.

PA (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.

PA (STON/) STONE D J.

PA (TAUP/) TAUPIER R J.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;

PI Stone DJ, Taupier RJ;

XX WPI; 2004-179665/17.

DR N-PSDB; ADO50847.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

PT atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and

XX in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; SEQ ID NO 10; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their

CC encoding polynucleotides. The invention is useful in diagnosing, treating

CC and preventing NOVX-associated disorders such as cardiomyopathy,

CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune

CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,

CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as

CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,

CC dyslipidaemias and other wasting disorders associated with chronic

CC diseases. The invention is also useful as hybridisation probes, in

CC chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. The invention is also useful in gene therapy and in the

CC preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 373 AA;

XX Query Match 28.2%; Score 62.5; DB 8; Length 373;

XX Best Local Similarity 33.9%; Pred. No. 39;

XX Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

XX

Oy

Db

RESULT 22

ADF44665

XX ADF44665 standard; protein; 375 AA.

XX ADF44665;

XX 12-FEB-2004 (first entry)

XX Human NOV1F protein SEQ ID NO:12.

XX human; antidiabetic; anorectic; cardiac; hypotensive;

XX antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;

XX protozoacide; antihelminthic; nootropic; neuroprotective;

XX antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;

XX antiinflammatory; dermatological; antiasthmatic; antipneumonic;

XX antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;

XX infectious disease; anorexia; cancer; cardiovascular disease;

XX hypertension; atherosclerosis; neurodegenerative disorder;

XX Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;

XX osteoarthritis; haematopoietic disorder; inflammatory skin disorder;

XX asthma; dyslipidaemia.

XX Homo sapiens.

XX WO2003066881-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-US003403.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 12-FEB-2002; 2002US-0356424P.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX 07-AUG-2002; 2002US-0401825P.

XX (CURA-) CURAGEN CORP.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;

PI Stone DJ, Taupier RJ;

XX WPI; 2003-748127/70.

DR N-PSDB; ADF44664.

XX New isolated NOVX polypeptides and polynucleotides, useful for

CC preventing, diagnosing or treating NOVX-associated disorders, e.g.

CC osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

CC asthma, or infections.

XX Claim 1; SEQ ID NO 12; 234pp; English.

XX The present invention describes an isolated polypeptide (I) comprising:

CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n

CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a

CC sequence that is at least 95% identical to (P), or having one or more

CC conservative amino acid substitutions in. (I) can be encoded by a nucleic

CC acid molecule (II), where the sequence is selected from the group

CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,

CC anorectic, cardiac, hypotensive, antiarteriosclerotic, anorectic,

CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,

CC

CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,
 CC osteopathic, antiarthritic, antiinflammatory, dermatological,
 CC antiasthmatic, antipneumonia, antidiabetic, antihypertensive, antitumor,
 CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules
 CC (II) and antibodies that immunospecifically bind (I), can be used in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease. They are useful for treating, preventing or diagnosing
 CC diseases such as metabolic disorders, diabetes, obesity, infectious diseases
 CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,
 CC cardiovascular diseases (hypertension, atherosclerosis),
 CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,
 CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,
 CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and
 CC (II) may also be used as targets for the identification of small
 CC molecules that modulate or inhibit e.g. neurogenesis, cell
 CC differentiation, cell proliferation, haematopoiesis, wound healing and
 CC angiogenesis, in gene therapy, in gene ration of antibodies that bind
 CC immunospecifically to (I) for use in therapeutic or diagnostic methods.
 CC (I) can also be used as hybridisation probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 375 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 375;
 Best Local Similarity 33.9%; Pred. No. 39;
 Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPPEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
 Db 176 AECGGCRNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTFGFCICPPG 231

RESULT 23

AD050850

ID AD050850 standard; protein; 375 AA.

AC AD050850;

XX

XX

DT 15-JUL-2004 (first entry)

XX

DE Human NOV1f protein.

XX

XX

KW NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

KW infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;

KW multiple sclerosis; anorexia; cancer-associated cachexia;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW haematopoietic disorder; dyslipidaemia; wasting disorder;

KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;

KW gene therapy; vaccine; human.

XX

OS Homo sapiens.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX (ANDE/) ANDERSON D W.
 PA (BURG/) BURGESS C E.
 PA (CASM/) CASMAN S J.
 PA (GORM/) GORMAN L.
 PA (JIWW/) JI W.
 PA (KEKU/) KEKUDA R.
 PA (LILL/) LI L.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (STON/) STONE D J.
 PA (TAUP/) TAUFIER R J.

Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;
 Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimketa RA;
 Stone DJ, Taupier RJ;

WPI; 2004-179665/17.
 N-PSDB; AD050849.

New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,
 PT atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and
 PT in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; SEQ ID NO 12; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their
 CC encoding polynucleotides. The invention is useful in diagnosing, treating
 CC and preventing NOVX-associated disorders such as cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
 CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune
 CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,
 CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as
 CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,
 CC dyslipidaemias and other wasting disorders associated with chronic
 CC diseases. The invention is also useful as hybridisation probes, in
 CC chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The invention is also useful in gene therapy and in the
 CC preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 375 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 375;
 Best Local Similarity 33.9%; Pred. No. 39;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPPEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37

Db 176 AECGGCRNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTFGFCICPPG 231

RESULT 24

ADC78324

ID ADC78324 standard; protein; 377 AA.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

antifungal; antiulcer; cytostatic; antipruritic; antiparkinsonian;
 neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
 neurotrophic; osteopathic; antiasthmatic; antiarthritic; antineumatic;
 antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;
 thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;

Qy 1 ADCNGAC-----SPEEVPPCRSRDC--RCVPFGLFV--GFCIHPTG 37
Db 176 AECPPGCRNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPG 231

Search completed: March 28, 2005, 08:57:12
Job time : 96 secs